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R04574 W40287

Derived amino acid Human TSP1 protein

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GenCore version 4.5
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Compugen Ltd.
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OM protein - protein search, using sw model

Run on: September 17, 1999, 03:03:09; Search time 64.1 Seconds (without alignments)
1.848 Million cell updates/sec

Title: Perfect score: US-09-037-657-1

Scoring table: Sequence: BLOSUM62 1 WSXWS 5

Searched: 188963 seqs, 23686106 residues

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT R06512

09-AUG-1990. 01-FEB-1990; U00635.

Erythropoietin; Diamond Blackfan anaemia; polycythemia vera. Homo sapiens. WO9008822-A.

EPO receptor.

04-JAN-1991 (first entry)

R06512 standard; protein; 508 AA, R06512;

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232 WSAWS 236

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R06511
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09-AUG-1990;
01-FEB-1990; U00635.
03-FEB-1989; US-306553.
(GENE-) GENETICS INST IN
                                                                                                                                                                                                      The sequence was deduced from DNA from a clone isolated from a cDNA library prepd. from uninduced murine erythroleukemia cells. It is a type I transmembrane protein with binding affinity for EPO. The gene and recombinant EPO receptor produced on expression of the DNA are used to develop reagents and systems to control and study erythropolesis. It is believed that the EPO receptor is dysfunctional in individuals with Diamond Blackfan anaemia, and
                                                                                                                                                  may be hyperactive in polycythemia vera. See also R06512 (human EPO receptor). Sequence 507 AA;
                                                                                                                                                                                                                                                                                                                                                                           Erythropoletin receptor and gene - used for developing reagents and systems to control and study erythropolesis.

Disclosure; Fig 1; 53pp; English.
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Erythropoletin; Diamond Blackfan anaemia; polycythemia vera.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'andrea A, Wong G;
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deduced from DNA from a clone isolated from
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                                    Score 30; DB 1; LC. Pred. No. 4.4e+02; No. 4.4e+02;
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                    Example: Fig 12: 24pp; German.

Example: Fig 12: 24pp; German.

The sequence is that of fusion protein GM-CSFRFc comprising the extracellular domain of granulocyte macrophage-colony stimulating factor (GM-CSF) fused via a hinge region to the Fc part of the heavy chain of human IgGl. It may be used as part of a cell free receptor binding test which can be used for the identification of agonists, antibodies, biological activity of soluble cellular antipodies, biological activity of soluble cellular antipodies.
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26-NOV-1991;
28-NOV-1990;
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The sequence was deduced from DNA obtd. from a clone isolated is commercially available human geenomic cDNA library in phage a commercially available human geenomic cDNA library in phage lambda Fix (Stratagene). The sequence encodes a type I transmembrane protein with binding affinity for EPO. The gene and recombinant EPO receptor produced on expression of the DNA are used to develop reagents and systems to control and study erythropolesis. It is believed that the EPO receptor is dysfunctional in individuals with Diamond Blackfan anaemia, and me be hyperactive in polycythemia vera.

See also R06511 (murine EPO receptor).
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(GENE-) GENET
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Cell free receptor binding test contg. recombinant comprising carrier bound to fusion partner coupled and second, labelled binding partner, for receptor
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Disclosure; Fig 2: 53pp: English.
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R10795;
25-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   following probe: a complementary RNA of the F3 CDNA of the rat prolactin receptor. One positive recombinant was isolated from the Hep G2 library, which was later used as a probe to rescreen the library. Five additional cDNAs were identified, and by combining two of the Six cDNAs, a PRL receptor cDNA of 2.5 kb was constructed, contg. a single ORF of 1866 bp. Similar partial length cDNA were isolated from the T47-D library.

Several regions of sequence identity between the human growth hormone and PRL receptors can be found, both in the extracellular and cytoplasmic domains.

The sequence is an important genetic engineering tool which may be used for the screening of growth hormone variants, for the development of the trace of the screening of growth hormone wallars.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of test kits to measure PRL receptor levels in human breast and prostate cancer biopsies, for the mesasurement of bioactive forms of prolactin, and for the development of drugs to induce stimulation or inhibition of
                              autoimmune
                                                      Granulocyte-macrophage colony-stimulating factor; myeloid leukaemia;
                                                                                                                     R10919;
08-MAY-1991
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N-PSDB; Q10550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kelly PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-1988; US-286445.
(ROYA-) ROYAL INST ADVAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
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cDNA of the
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antibody
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Query Match
Best Local Similarity
Aches 4; Conserv
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10-AUG-1990; AUG-005743.
11-AUG-1989; AUG-005743.
08-MAY-1990; AUG-000014.
(AMRA-) AMRAD CORP LTD.
                                                                                                                                                                                                                                             k22228 standard; protein;
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                             6-AUG-1991; U05856.
7-AUG-1990; US-568936.
GETH ) GENENTECH INC.
Bass SH, Cunningham BC,
                                                                                                                                                                    runcated human prolactin binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         urposes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ecombinant or synthetic receptor for granulocyte-macrophage olony - used for treatment and diagnosis or related diseases, g. myeloid leukaemia or auto-immune reactions laim 1; Fig 6B; 85pp; English and the combined cDNAs of pGNR138 and SMR29 which were isolated from a cDNA library prepd. from hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09102063-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acental RNA. The DNA care prodn. of recombinant
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92-096838/12
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                                                                                                                                                          ligand complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to study the mechanism
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= N-glycosylation site 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= N-glycosylation site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label N-glycosylation site
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                                                                                                                                                                                                                                                                                                                                                                                                                             96.8%;
                             Fuh G, Lowman HB, Matthews DJ;
                                                                                                                                                                                                                                               211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from the combined cDNAs of pGMR138 and
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30;
Pred. No.
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3.5e+02;
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This truncated human prolactin binding protein is encoded by the insert contained in plasmid phPRLbp(1-211). The hPRLbp gene fragment is transcribed under the control of the alkaline phosphatase promoter and secreted into the host (E.coli) periplasm under the direction of the stII signal sequence. A stop codon and MiuI restriction site were introduced after the threonine 211 codon which inmediately precedes the transmembrane domain of the receptor. The plasmid was used as a template for site-directed mutagenesis to modify the metal-chelating centre of the protein. See e.g. R24273
               MPLV env-vmpl fusion protein.
                                                                                                                                                                                                                                                                                                                                                                 Plasmid phPRLbp(1-211) (see R22228) coding for truncated, soluble prolactin binding protein was mutagenised such that the His codon at position 188 was substituted by an Ala codon. The hPRLbp variant has altered binding affinity for hGH.
                                                                                                                                                                                                                                                                                                                                                                                                                         lactogenic and somatogenic response Claim 41; Page 56; 74pp; English. Plasmid phPRLbp(1-211) (see R22228)
                                           05-NOV-1992
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New method of modifying polypeptide hormone-receptor complex produce human growth hormone variant, useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wells
                                                               R23971 standard; Protein; 284 AA.
R23971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-AUG-1991; U05856.
17-AUG-1990; US-568936.
(GETH ) GENENTECH INC.
Bass SH, Cunningham BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 92-096838/12.
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for an example of a preferred variant.
Sequence 211 AA;
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4; Conserv
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                                                                                                                                                                                                                                                        Conservative
                                           (first entry)
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man prolactin binding protein variant
nan prolactin binding protein variant
cheiate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "wild-type His replaced
leukaemia virus; envelope protein; F-MuLV;
                                                                                                                                                                                                                                                                        96.8%;
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Pred. No.
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Pred. No.
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t, useful for stimulating
                                                                                                                                                                                                                                                                    DB 1; ;
1.8e+02;
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Best Local S
Matches 4
N-PSDB; Q24674.

Polypeptides similar to v-mlp protein or mruv treatment of myeloproliferative diseases.

Claim 1, Page 28; 75pp; French.

This polypeptide is encoded by clone MPLV107, isolate genomic bank prepared from clones of Mus dunni cells a unique copy of the MPLV provirus. The bank was screa unique copy of the MPLV provirus.
                                                                                                                                                                                                             05-NOV-1992
                                                                                                                        30-APR-1992.
19-OCT-1990;
19-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                        Polypeptides similar to v-mlp protein of MPLV - f treatment of myeloproliferative diseases Claim 8; Fig 28; 75pp; French.

The rearranged env MPLV gene has an open reading acids and deduced mol.wt. of 31kD. The env-vmpl f comprises the N-terminal 64 amino acids from F-ML the signal peptide, 36 amino acids from the centre F-MLTV env gene and 184 amno acids specific to MF See R23970, 024674-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-1992.
19-OCT-1990; WO-F0762.
19-OCT-1990; WO-F07623.
19-OCT-1990; WO-F07623.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
Charon M, Gisselbrecht S, Penciolelli JF, Souy
Tambourin P, Varlet P, Vigon I, Wendling F;
                                                                                            (INRM ) INSERM INST NAT
Charon M, Gisselbrecht (
Tambourin P, Varlet P, V
                                                                                                                                                                                          MPLV env protein with growth factor Myeloproliferative leukaemia virus; Myeloproliferative leukaemia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 92-167154
N-PSDB; Q24677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Friend replication competent ecotropic Myeloproliferative leukaemia virus
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                                                                                                                                                                                                                                                                                            WSAWS
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4; Conser
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WO-F07623.
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                                                                                                                                                                                                                                            protein;
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- "from F-MuLV"
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                                                                                            T SANTE & RECH MEDICALE.
S, Penciolelli JF, Souyri
Vigon I, Wendling F;
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Pred.
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from the central
specific to MPLV.
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2.5e+02;
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                                     isolated
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Query Match
Best Local S
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See R23971 and Q2
Sequence 635 AP
  19-OCT-1990; F00762.
19-OCT-1990; WO-F07623.
(INEM ) INSERM INST NAT S
Charon M, Gisselbrecht S,
Tambourin P, Varlet P, Vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             env protein having the amino acid sequence assigned GENESEQ accession number R23970. The protein is involved in the ligand-fixing or signal-transmitting function of haematopoietic growth factor receptors; is recognised by antibodies to the protein R23970; when produced from the MPLV genome it can induce the protein R23970; when produced from the MPLV genome it can induce the protein R23970; when produced from the MPLV genome it can induce the matter of the mat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promote proliferation of haematopoietic cells in differentiation of haematopoietic cells. See also Q24674-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INRM.) INSERM INST NAT
Charon M, Gisselbrecht S
Tambourin P, Varlet P, V
WPI; 92-167154/20.
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Myeloproliferative leukaemia virus;
haematopoletic cell; Growth Factor r
Myeloproliferative leukaemia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides similar to v-mlp protein of treatment of myeloproliferative diseases Claim 3; Page 30; 75pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R27659;
05-NOV-1992 (first
                                                                                                                                                                                                                         Partial MPLV-env related polypeptide.
Myeloproliferative leukaemia virus; envelope protein;
haematopoletic cell; Growth Factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; Q24675
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                                                                                                                                                                                                                                                                                                              05-NOV-1992 (first entry)
                                                                                                                                                                                                    Myeloproliferative leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L9-OCT-1990; F00762.
L9-OCT-1990; WO-F07623
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                                                                                                                                                                                                                                                                                                                                                                      standard;
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d Q24674-7.
5 AA;
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                                                                                                                                                                                                                                                                                                                                                                      Protein;
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T SANTE & RECH MEDICALE.
S, Penciolelli JF, Sous
Vigon I, Wendling F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T SANTE & RECH MEDICALE.
S, Penciolelli JF, Souyri
Vigon I, Wendling F;
                                                                                                                                                                                                                                                                                                                                                                         184
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3.3e+02;
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5.5e+02;
     , Souyri
F;
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involved
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Query Match

Score 30; DB 1;

Length 507

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment of myeloproliferative diseases

PT treatment of myeloproliferative diseases

PS Claim 4; Page 31; 75pp; French.

CC This polypeptide is an example of a fragment related to the MPLY

CC env protein having the amino acid sequence assigned GENESEQ

CC accession number R23970. The protein is involved in the

CC ligand-fixing or signal-transmitting function of haematopoletic

CC growth factor receptors; is recognised by antibodies to the

CC protein R23970; when produced from the MPLY genome it can induce/

CC promote proliferation of haematopoletic cells and/or is involved

CC see also 024674-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                    Disclosure; Fig 2; 24pp; English.

Mouse erythroleukaemia (MEL) cells were used to construct a cDNA library. The cDNA was used to transfect COS-1 cells and these were screened for radioiodinated erythropoletin (EPO) binding to isolate cDNA encoding the EPO receptor. The cDNA may be used to isolate the EPO receptor from other sources to study, treat or diagnose disorders in which the EPO receptor is dysfunctional. The EPO receptor may also be used to raise antibodied or for treating hypersensitivity to EPO or who have elevated levels of EPO. The por
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS5278065-A.
                                                                                                                                                                                                                                                                                                                                                                                                         CHIL-) CHILDRENS MEDICAL CENT.

GEMY ) GENETICS INST INC.

WHED) WHITEHEAD INST BLOMEDICAL RES

Yandrea A, Jones SS, Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-JAN-1994.

13-FEB-1989; 306503.

13-FEB-1989; US-306503.

15-MAR-1991; US-678877.
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N-PSDB; Q24676.
                                                                                                                                                                                                                                                                           ecombinant DNA encoding erythropoletin receptor - used to evelop prods. for study, treatment or diagnosis of disorders in hich receptor is dysfunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 WSAWS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                          pref. used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WSXWS
secondary polycythemia also R47518.
                                                                                                                                                                                                                                                                                                                                                                                     94-025409/03.
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75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "potential N-glycosylatiom site"
250. .271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "putative transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "mature EPO receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30;
Pred. No.
                                primary proliferative polycythemia
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1.6e+02;
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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19-OCT-1994 (first entry)

Mouse soluble EPO receptor protein fragment.

Murine; soluble; erythropoletin; EPO; receptor protein; sEPO-R;

antigen; diagnostic agent; blochemical reagent.

Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        develop prods. for study, treatment or diagnosis of disorders in which receptor is dysfunctional Disclosure; Fig 9; 24pp; English.

Mouse erythroleukaemia (MEL) cells were used to construct a cDNA ilbrary. The cDNA was used to transfect COS-1 cells and these were screened for radioiodinated erythropoietin (EPO) binding to isolate cDNA encoding the EPO receptor. This cDNA was used as a probe to screen a human genomic cDNA library to obtain DNA encoding the human EPO receptor. The cDNA may be used to study, treat or diagnose disorders in which the EPO receptor is disprinctional. The EPO disorders in which the EPO receptor is disprinctional. The EPO
                                                                                                              R50326 standard; Protein; 265 AA.
                                                                                                                                                                                                                                                                                                                                                                                        hypersensitivity to EPO or who have is pref. used for treating anaemias, and secondary polycythemia. See also R47517.
Sequence 508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor may also be used to raise antibodied or for treating hypersensitivity to EPO or who have elevated levels of EPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D'andrea A, Jones
WPI; 94-025409/03.
                                                                                                                                                                                                                233 WSAWS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHIL-) CHILDALI, (GEMY) GENETICS INST INC. (WHED) WHITEHEAD INST BIOMEDICAL (WHED) Tones SS, Wong GG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region
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4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251. .272
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15-FEB-1994.
04-MAR-1992;
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Soluble erythropoletin receptor protein - and DNA coding for SEDO-R, useful as diagnostic reagent Disclosure; Page 5-6; 9pp; Japanese. This sequence represents a fragment of the murine soluble erythropoletin (EPO) receptor protein (SEPO-R). This protein is able to bind to EPO and has antigenicity as an EPO receptor. The molecular wieght of the full length protein is pref 33 or 29 kD. The protein is useful as a drug, as a diagnostic agent and a blochemical reagen sequence 265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
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232 WSAWS 236
                                                                                                                                                                                                     Disclosure: Fig 1: 9pp; Japanese. This sequence represents the murine soluble erreceptor protein (sEPO-R). This protein is all has antigenicity as an EPO receptor. The mole full, length protein is pref 33 or 29 kD. The drug, as a diagnostic agent and a biochemical sequence 507 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R50327 standard; Protein; 507 AA. R50327; 19-OCT-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     15-FEB-1994.
04-MAR-1992; 082865.
04-MAR-1992; JP-082865.
(SNOW ) SNOW BRAND MILK PROD CO LTD (SNOW ) SNOW BRAND MILK PROD CO LTD WPI; 94-094847/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse soluble EPO receptor protein Murine; soluble; erythropoletin; EPO; nantigen; diagnostic agent; blochemical Mus musculus
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04-MAR-1992; JP-082865.
(SNOW) SNOW BRAND MILK PROD CO LTD.
WPI; 94-094847/12.
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232 WSAWS 236
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coluble erythropoietin receptor protein - and DNA coding for EPO-R, useful as diagnostic reagent
                                           1 WSXWS 5
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75. .77
/note= "N-linked glycosylation site"
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/note-_ "Signal peptide"
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                                                                                                            96.8%; Score 30; DB 1;
80.0%; Pred. No. 4.4e+02;
                                                                                                                                                                                                                         the murine soluble erythropoletin (EPO). This protein is able to bind to EPO and PO receptor. The molecular wieght of the ref 33 or 29 kD. The protein is useful as a ent and a biochemical reagent.
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Pred. No. 2.3e+02;
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Search completed: September 17, 1999, 03:08:10

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Title: Perfect score: Sequence:

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Scoring table:

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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS9_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*

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PCT US95-01775-17 PCT-US95-04570-47 PCT-US95-04589-47 PCT-US95-16626-7 US-07-646-531D-15 US-07-797-556-2 US-07-797-556-6 US-07-862-021B-12 US-07-862-021B-12 US-07-862-021B-14 US-07-862-021B-14 US-07-862-021B-14 US-07-862-021B-14 US-07-943-843-4

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US-08-184-327A-4
US-08-184-327A-8
US-08-285-0-859-17
US-08-351-149-6
US-08-351-149-6
US-08-449-329-13
US-08-449-329-13
US-08-449-329-13
US-08-449-828-17
US-08-313-288B-17
US-08-313-288B-17
US-08-445-073-13
US-08-445-073-13
US-08-445-073-13
PCT-US91-03896-13
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RESULT 2
US-07-676-647-13
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
15-07-676-647-10
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Matches
 GENERAL INFORMAPPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA:
SOFTWARE: PATENTIA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/676,647
FILING DATE: 19910328
CLASSIFICATION: 5.14
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELEPHONE: 212 790-900
TELEPHONE: 212 790-900
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APPLICANT: Squinto, Stephen P.
APPLICANT: Furth, Mark E.
APPLICANT: Yancopoulos, George I
TITLE OF INVENTION: The Ciliary
NUMBER OF SEQUENCES: 15
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                                                                                                                      WSAWS 185
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                                       INFORMATION:
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4; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
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New York
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                                    PatentIn Release #1.0, Version #1.25
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OLECULE TYPE: protein
                                                              474 WSSWS 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466 WSAWS 470
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                                                                                     1 WSXWS 5
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                                                                                                                                                                                       LECULE TYPE:
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                                                                                                                         Similarity
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                                                                                                                                                                                                                           635 amino acids
                                                                                                                                                                                                                                                                                           ON NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi, Esther S
                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
ication US/08184327A
                                                                                                                                                                                                                                                                                                                  PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                            Amgen Inc.,
                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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                                                                                                                                                                                                                                                                                          US/08/184,327A
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Pred. No.
                                                                                                                                    Score 30;
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                                                                                                                                    Length 635;
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Choi, Esther S. Hokom, Martha M.

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JS-08-250-859-17
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Best Local Similarity bu...
Conservative
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INFORMATION FOR SEQ ID NO: {
SEQUENCE CHARACTERISTICS:
LENGTH: 482 amino ....
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ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
ORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466 WSAWS 470
                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, URRENT APPLICATION DATA:
                                                                                                            CLASSIFICATION: 435
TTORNEY/AGENT INFORMATION:
                                                             NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 94-2
                                                                                                                                                                                                                                                                                                             STREET: 422.
                                                                                                                                                                                                                                                                                                                                                                                                            TLE OF INVENTION:
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                                                                                                                                                                                                      OMPUTER: IBM FO
                           ECOMMUNICATION INFORMATION:
ELEPHONE: 206-547-8080 ext 322
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                                                                                                                                                               CATION NUMBER:
                                                                                                                                                                                                                                                                               98105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08250859
                                                                                                                                                                                                                                                                                                                                       E: ZymoGenetics, Inc.
4225 Roosevelt Way, N.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Amgen Inc., U.S. Patent Operations/RRC
1840 DeHavilland Drive
                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                      Burkhead, Steven K.
VENTION: METHOD FOR PREPARING ORPHAN RECEPTOR LIGANDS
                206-632-4009
                                                                                                                                                                                                                                                                                                                                                                                                                                           Holly, Richard D
                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No.
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OS-08-351-149-6
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                                                             Matches
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306 WSSWS 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473 WSAWS 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: Improvements in Granulocyte-Macroph ITLE OF INVENTION: Colony-Stimulating Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 RRENT APPLICATION DATA:
                              1 WSXWS 5
                                                                           Local
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                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/351,149
FILING DATE: 23-NOV-1994
CLASSIFICATION: 530
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DIUM TYPE: Floppy
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: D.C.
RY: U.S.A.
                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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Colony-Stimulating Factor Receptor and Derivatives Thereof
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                                                                                                                                                                                                                                                                                                    30,353
                                                                         Score 30; DB 1;
Pred. No. 3e+02;
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                                                                                     Length 400;
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                                                      Gaps
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US-08-243-010-6

Sequence 6, Application US/08243010 Patent No. 5639597

INFORMATION

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; MOLECULE TYPE:
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                  1 WSXWS 5
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ING DATE: 26-NOV
LICATION NUMBER:
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                                                          New York
READABLE FORM:
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                                                                      1155 Avenue of the Americas
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1300 I Street, N.W.
                              U.S.A.
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                                                                                                                                          soluos,
                                                                                                                                                                                   , Samuel
                                                                                                                                                         Mark E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carol P
                                                                                                                       The Ciliary Neurotrophic Factor Receptor
                                                                                                                                                                       Stephen P.
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                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,677
FILING DATE: 15-MAY-1991
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                                           ATTORNEY/AGENT INFORMATION
                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
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                                                                                                       CLASSIFICATION: 530
                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                OPERATING SYSTEM:
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FILING DATE: 15-MAY-1991
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                                                                                                                                                               PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                     .155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
E: peptide
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VISTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.
               NUMBER:
                                                                                                                                                                                                             Floppy disk
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he Ciliary Neurotrophic Factor Receptor
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6526-065
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Pred. No.
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ON FOR SEQ ID NO:

13:

212 790-9090

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Best Local Similarity 80.0
4; Conservative
                                                                                                                 MOLECULE TYPE:
-08-490-803-17
                                                                Query Match
Best Local Similarity
                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -490-803-17
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
473 WSAWS 477
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STRANDEDNESS: si
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                          1 WSXWS 5
                                                                                                                                                                                                                            ECOMMUNICATION INFORMATION: ELEPHONE: 206-547-8080 ext 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                     STRATION NUMBER:
                                                                                                                                                                                                                                                                                              SIFICATION: 435
EY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      ICATION NUMBER:
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5705349
                                                                                                                                                           amino acid
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Roosevelt Way, N.E.
                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Richard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHOD FOR PREPARING ORPHAN RECEPTOR LIGANDS
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                                                                                                                                                                                                                                                         94-2
                                                                Score 30;
Pred. No.
                                                                          Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 185;
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RESULT 12

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                                                                                                                                                                                    ent No.
                                                                                                                                                                                                                                                                        306 WSSWS 310
OMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                  1 WSXWS 5
                                                                                                                                                                                                                                                                                                                                                                                                                    ECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASSIFICATION: 435
R APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIUM TYPE: Floppy disk
MPUTER: IBM PC compatible
ERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TER READABLE FORM:
IUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LICATION NUMBER: US/01
ING DATE: 07-FEB-1995
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NG DATE: 23-NOV-199/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
                                                        New York
                                        New York
                                                                                                                                                                                                Application US/08313288B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L.
4R: 30,353
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Colony-Stimulating
                                                                                                                           NOVEL SECRETED
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                                                                                                                        EXPRESSION AND USES OF A CRETED PROTEIN, F-SPONDIN
                                                                                                                                                                                                                                                                                                                             Mismatches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 545 WSSWS 549
                                                                                                                                                                                                                                       DAPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM compatible
                                                                PPLICATION NUMBER: 08/1
ILING DATE: 16-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECOMMUNICATION INFORMATION: CLEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
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[LING DATE: Janua:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WSXWS 5
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                                                                                       ICATION NUMBER: 08/4
ING DATE: 07-JUL-1995
APPLICATION DATA:
                                                                                                                SIFICATION:
APPLICATION DATA:
08/499,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                          CATION NUMBER:
                                                                                                                                                                                                TING SYSTEM: DOS
ARE: FastSEQ for Windows Version
APPLICATION DATA:
                          DATE: 16-AUG-1330/AGENT INFORMATION: Ellinger, Mark S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 80.
4; Conservative
                                                                                                                                                                                                                                                                                                                                   Minneapolis
NCE/DOCKET NUMBER: 07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08850293
                                                                                                                                                                                                                                                                                                                                                E: Fish & Richardson P.C., P.A. 60 South Sixth Street, Suite 3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acids
                                                                                                                                                                     05-MAY-1997
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DN: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391-0526
                                                                                                                                                                                                                                                                                                                                                                                                        PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DATA
                                                                              08/106,815
                                                                                                                                                                                   US/08/850, 293
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    07004/002001
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В

181 WSAWS 185

1 WSXWS 5

Query Match Best Local Similarity

96.8%;

Score 30; Pred. No. 1

Length 185;

Indels

0;

Conservative

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Query Match
Best Local Similarity
                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                       TELEPHONE: 212 790-9090
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 WSAWS 237
                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
DERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WSXWS 5
                                                                                                                                                               STRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         10036
                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08445073
                                                                                                                                                                                                                                                                                                                                                                                                                         1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Squinto, Squinto, Mark E.
                                                                                                                                                                                                                                                                        ON NUMBER:
                                                                                                                                                                                                                                                ION:
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peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.8%;
                                                                                                                                                                                                                  US 07/676,647
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Search completed: September 16, 1999, 20:41:05

Job time: 9424 sec

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Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein search, using sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR_60:*
1: pir1:
2: pir2:
3: pir3:
4: pir4:
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31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122810 seqs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd
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pir2:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 )7 ; Search time 49.27 Seconds
(without alignments)
4.056 Million cell updates/se
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MPL-K protein prec
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complement C6 prec
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Result No.

622 2 A40144 prolactin receptor 625 2 S35317 hematopoletic grow 432 2 I48343 interleukin-I1 rec 437 2 S05478 properdin - mouse 626 2 S37622 proto-oncogene - m 367 2 G71178 hypothetical prote
A40144 S35317 I48343 S05478 S37622 G71178
prolactin receptor hematopoietic grow interleukin-11 rec properdin - mouse proto-oncogene - m hypothetical prote
prolactin receptor hematopoletic grow interleukin-11 rec properdin - mouse proto-oncogene - m hypothetical prote

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A:Note: sequence modified after extraction from NCBI backbone A;Note: the authors translated the codon GAT for residue 31 as B A;Note: an insert compared to other published sequences is considered by authors as R;Maouche, L.; Tournamille, C.; Hattab, C.; Boffa, G.; Cartron, J.P.; Chretien, S. Blood 78, 2557-2563, 191
A;Title: Cloning of the gene encoding the human erythropoletin receptor. A;Reference number: 152563; MUID:92399734
A;Accession: 152563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Penny, L.A.; Forget, B.G. Genomics 11, 974-980, 1991
A;Title: Genomic organization of the human erythropoietin receptor gene. A;Reference number: A55280; MUID:92147143
A;Accession: A55280
A;Cross-references: GDB:125242;
A;Map position: 19p13.3-19p13.2
                                                                                                           A; Gene: GDB: EPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-508 <EHR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: The erythropoietin receptor gene: cloning and identification of multiple tra
A; Reference number: A53958
A; Accession: A53958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Cloning of the human erythropoietin receptor gene.
A;Reference number: A49824; MUID:92399733
A;Accession: A49824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Homo sapiens (man)
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                                                                                                                                                                                                 ;Molecule type: DNA :Residues: 1-96 <RES> ;Cross-references: GB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Status: not compared with conceptual translation ;NoLecule type: mRNA; DNA ;Residues: 1-101; R',103-188, 'RP',191-243, 'E',245-508 <WIN>;Noguchi, C.T.; Bae, K.S.; Chin, K.; Wada, Y.; Schechter, A. lood 78, 2548-2556, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lood 76, 24-30, 1990
|Title: The gene for the human erythropoletin receptor: analysis of the coding seque
|Reference number A60160; MUID:90304334
|Accession: A60160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:M60459; NID:g182244; PID:g182245; Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget,
                                                                                                                                                                                                                                                                                                                                                             Status: translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: sequence
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;Date: 12-Feb-1993 *sequence_revision 05-Ap;
Accession: A43799; A60160; A49824; A53958;
Jones, S.S.; D'Andrea, A.D.; Haines, L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type:
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                                                                                                                                                                                            GB:M76595; NID:g182147; PID:g553281
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                                                OMIM:133171
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A53958; A55280; I52563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      backbone (NCBIN:113293, NCBIP:113294)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forget, B.G.; Jenkins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               z
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erythropoletin receptor precursor, membrane-bound form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 05-Apr-1995 #text_change 05-Sep-1997
C;Accession: A41686; A32385; S13249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   닭
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;76/Binding site: carbohydrate
                                                                                                                                                                                                                          Superfamily: erythropoietin receptor; cytokine receptor homology Keywords: alternative splicing; cytokine receptor; elycoprotein; 1-24/Domain: signal sequence #status predicted <SIG>25-507/Product: erythropoietin receptor #status predicted <WAT>25-249/Domain: extracellular #status predicted <EXT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reference number: S13249;
Accession: S13249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:J04843; NID:g193090; PI
Experimental source: murine erythroleukemia
Kuramochi, S.; Ikawa, Y.; Todokoro, K.
Mol. Biol. 216, 567-575, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                        32-238/Domain: cytokine receptor homology <CRS>
350-271/Domain: transmembrane *status predicted <TMM>
772-507/Domain: intracellular *status predicted <INT>
72-62,90-106/Disulfide bonds: *status predicted
75/Binding site: carbohydrate (Asn) (covalent) *status
                                                                                                                                                                                                                                                                                                                                                                                                      Experimental source: murine
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                                                                                                                                                                                                                                                                                                                                                   introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3
                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-507 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           litle: Expression cloning Reference number: A32385; Recession: A32385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lno, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.
Cell. Biol. 11, 5527-5533, 1991
'itle: Unregulated expression of the erythropoietin receptor gene caused by
eference number: A41686; MUID:92017832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             esidues: 1-507 <DAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           esidues:
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kperimental source: murine erythroleukemia (MEL) cell 
Andrea, A. D.; Lodish, H.F.; Wong, G.G. 
157, 277-285, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-272/Domain: transmembrane #status predicted 73-508/Domain: intracellular #status predicted 7-62,91-107/Disulfide bonds: #status predicted 6/Binding site: carbohydrate (Asn) (covalent) #
                                                                                                                                                                                                                                                                                                                                                                                                                    oss-references: EMBL:X53081; NID:g50861; PID:g50862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237/Region: WSXWS motif
                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Characterization
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    Similarity
4; Conser
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       Conservative
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                             96.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the murine erythropoietin MUID:89195238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   murine erythropoletin receptor genes MUID:91080149
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Score 30; DB
Pred. No. 2.7e
0; Mismatches
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Pred. No. 2.7e
0; Mismatches
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                        DB 1;
2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:g309219
ia (MEL) cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
2.7e+02;
                                                                                                               #status
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                                           Length 507
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                                                                                                               predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      line F5-5
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                                                                                                                                                                                                                                                                                                     transmembrane
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                                                                               A; Introns: 28/1; 69/3; 136/1; 170/3;
                                                                                                                                                                    A;Cross-references: GB:S47168; NID:g258527; PID:g258529
A;Note: sequence extracted from NCBI backbone (NCBIN:116668,
A;Note: authors translated the codon CTA for residue 642 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   당
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                                 A; Description: required for guidance of pioneering axons
                                                                                                               A;Gene: unc-5
                                                                                                                                                   A; Note: mRNA lacking
                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-947 <LEU>
                                                                                                                                                                                                                                                                                                                   A; Reference number: A44294; 1
A; Contents: variety Bergerac
                                                                                                                                                                                                                                                                                                A; Accession: B44294
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                                                                                                                                                                                                                                                                                                                                                                 ;Title: UNC-5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contains: unc-5 protein, short form Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                               Leung-Hagesteijn,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: B44294; A44294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein,
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long form - Caenorhabditis elegans

1993 #sequence_revision

28-Jul-1995

#text_change 20-Mar-1998

a transmembrane

MUID: 93046629

the first exon is equally prevalent

Val; sequence

NCBIN: 110 shown fol:

229/1; 351/2; 581/1; 886/3

glycoprotein;

and cells migrat

1992

C.; Spence, A.M.; Stern, B.D.; Zhou, Y.; Su, M.W.; Hedgecock,

and

thrombospondin type

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F;43,437/Binding site: carbohydrate
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                                                                                                                                                                                          Matches
                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: part of the sequence was confirmed by prote: Comment: CB, a constituent of the cytolytic (memb) Comment: The alpha chain binds to the beta chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
Residues: 1-583 <RAO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rao, A.G.; Howard, O.M.Z.; Ng, S.C.; Whitehead, ochemistry 26, 3556-3564, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Date: 28-Dec-1987 #sec
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544 WSSWS
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                                                                                             1 WSXWS 5
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                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                      Score 30; DB 1;
Pred. No. 3.1e+02
                                                                                                                                                                                                                                                                                                                                                                                                           (Asn)
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(membrane attack)
chain, gamma chain,
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                                                                                                                                                                                                                                                                    Length 583
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                                                                                                                                                                                                                                                                                                                                                                                                  predicted
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                                                                                                                                                                                                                     Nol. Gen. Genet. 232, 335-343, 1992
A;Title: The lysozyme locus in Drosophila
A;Reference number: S20914; MUID:92269751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  erredoxin--NADP+ reductase (EC 1.18.1.2) precursor -
                                           Reference number: S41573
Accession: S41576
                                                                                            Cross-references: EMBL:X58382; NID:g8197; Daffre, S.; Kylsten, P.; Samakovlis, C.; Longen, Genet. 242, 152-162, 1994
                                                                                                                                                               Molecule type: DNA Residues: 1-140 <KYL>
                                                                                                                                                                                                                                                                                                                     Species: Drosophila melanogaster
Date: 03-Feb-1994 #sequence_revision 03-Feb-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: human ferredoxin--NADP+ reductase Keywords: FAD; mitochondrion; NADP; oxidoreductase Keywords: transit peptide (mitochondrion) #status predicted <TNP>
                                                                             Title: The lysozyme locus
                                                                                                                                                                                                        Accession:
                                                                                                                                                                                                                                                                                    Kyısten,
                                                                                                                                                                                                                                                                                                         Accession: S20914; S4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Mus musculus (house mouse)
Date: 15-Feb-1996 #sequence_revision 08-Nov-1996 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:D49920; NID:g1088468; PID:g1088469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reference number: Accession: S60028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ochim. Biophys.
Title: cDNA clo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residues: 1-494 <ITO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toh, S.; Iemura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55-390/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -494/Product:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3-211/Domain: immunoglobulin homology <IG2>
9-300/Domain: thrombospondin type 1 repeat homology #status atypical <THR1>
1-354/Domain: thrombospondin type 1 repeat homology <THR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 WSSWS
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Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 WSAWS 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WSXWS 5
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                                                                                                                                                                                                                                                                                  P.; Kimbrell, D
1-140 <DAF>
                                         S41576
                                                                                                                                                                                                        S20914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamada, E.; Yoshimura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.8%;
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                                                                                                                                                                                                                                                               A.; Daffre, S.; Samakovlis, C.; Hultmark, D.
343, 1992
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                                                                         Drosophila melanogaster: an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB
Pred. No. 2.6e
0; Mismatches
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6e+02;
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                                                                                                                                                                                                                                                                                                                     #text_change 08-Sep-1997
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                                                                                       C;Accession: S41574; S32643;
R;Daffre, S.; Kylsten, P.; St
Mol. Gen. Genet. 242, 152-16;
A;Title: The lysozyme locus 1
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                                                      A; Reference number: S41573
A; Accession: S41574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Superfamily: lysozyme c;Reywords: bacteriolytic enzym;Reywords: signal sequence;1-18/Domain: signal sequence
                                                                                                                                                            Date: 25-Dec-1994 #sequence
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;Daffre, S.; Kylsten, P.; Sam
ol. Gen. Genet. 242, 152-162,
                                                                                                                                                                             Species:
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Best Local
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4; Conserv
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EMBL: 222225; NID: g289001; PID: g289002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: Z22226; NID: g296038; PID: g296039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ytic enzyme; glycosidase;
                                                                                                                                                                                                                                                                                                                                                      96.8%; Score 30; DB
80.0%; Pred. No. 81;
Live 0; Mismatches
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                                                                                                                        Samakovlis, C.;
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                                                                                     Drosophila melanogaster:
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#status predicted <SIG>
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Pred. No.
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81;
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lysozyme (EC 3.2.1.17) X - fruit fly (Drosophila melanogaster) (fragment) C;Species: Drosophila melanogaster C;Date: 25-Dec:1994 #sequence_revision 19-Oct-1995 #text_change 24-Sep-1998
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                                                                                   RESULT
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Keywords: bacteriolytic enzyme; glycc
1-18/Domain: signal sequence #status
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Genetics: LSYC
Genetics: <LYSB>
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              Accession:
                                                                                                                                                                                            Query Match
Best Local
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Best Local
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Residues: 1-140 <DAF>
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25-Dec-1994 #sequence_revi
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              S41580;
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Samakovlis,
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Pred. No.
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Pred. No. 81;
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                                                                                                                                                                                                                                                                              polysaccharide
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R;Delius, H.; Hebling, U.; submitted to the Protein S

; Hofmann, B. Sequence Database, July 1996

\$59000;

Date: 12-Jul-1996 #sequence. Accession: S67305; S67306; S Species: Saccharomyces cerevisiae Date: 12-Jul-1996 #sequence_revis

N; Alternate names:

hydratase (EC 4.2.1.11) ERRI - yeast (Saccharomyces cerevisiae) es: ERR2 protein; protein 06788; protein P0304; protein YOR393w;

org

revision 12-Jul-1996 #text_change

nosphopyruvate

A; Molecule type: DNA A; Residues: 1-330 A; Reference number: S67261 A; Accession: S67305

A; Experimental source: strain

Wedler,

A;Cross-references: EMBL: Z75301; MIPS:YOR393w

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C;Superfamily: enclase
C;Keywords: carbon-oxygen lyase; gluconeogenesis;
F;40/Binding site: magnesium 2 (Ser) #status predicted
F;212,346/Active site: Glu, Lys #status predicted
F;247,296,321/Binding site: magnesium 1 (Asp, Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 3
C; Superfamily: lysozyme c
C; Keywords: bacteriolytic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: lysP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-81 <DAF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number:
                                                                                                                                                                                                                                                                                  A; Molecule type:
                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                Churcher,
                                                                                                                                                                                                                                                                                                                                                                                                         osphopyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL: Z22224; NID: g288922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ol. Gen. Genet. 242, 152-162, Title: The lysozyme locus in
                                                            Matches
                                                                                                                                                                                                                          Map position: 13R
                                                                                                                                                                                                                                                                                                                  Reference number:
                                                                                                                                                                                                                                                                                                                                                              Accession:
                                                                                                                                                                                                                                                                                                    Accession: S69881
                                                                                                                                                                                                                                                                                                                                  mitted to
                                                                                                                                                                                                                                                       cos-references:
304 WSSWS
                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 WSAWS
                                                                                                                                                                                                                                                                                                                                                                            06-Sep-1996
                             1 WSXWS
                                                                                                                                                                                                              YMR323w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMXSM
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umber: S69876
   308
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                                                                                                                                                                                                                                                      EMBL: Z54141; NID: g1072408; PID: g1072413; MIPS: YMR323w
                                                                                                                                                                                                                                                                                                                                                                            #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                             cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.8%;
                                                                        96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme; glycosidase; hydrolase; polysaccharide degradatic
                                                                                                                                                                                                                                                                                                                                                                                                        (EC 4.2.1.11) YMR323w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                Library,
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                                                                       Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                  November
                                                                                                                                                                                                                                                                                                                                                                            06-Sep-1996 #text_change 22-May-1998
                                                                                                                               tatus predicted predicted (Asp, Glu, Asp) #status
                                                                       DB 2;
2.3e+02;
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icted
                                                                                     Length 437
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                                                          Indels
                                                                                                                                                                             hydro-lyase;
                                                                                                                                  predicted
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Species: Mus musculus (house mouse)
Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 17-Mar-1999
Accession: A44090; A26489; B23159
                                                                                                                                                                                   lacental lactogen II precursor - mouse
                                                                                                               Shida, M.M.;
                                                       Reference number:
                                                                         Title: Placental-specific
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                 Matches
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10/Binding site: magnesium 2 (;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ene: SGD:ERR2
Pross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                >elius, H.; Hebling, U.
mitted to the Protein Sequence Database, May 1996
teference number: S64967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ererence number: S65292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               volecule type: DNA
Residues: 120-230,'K',232-437 <PRK>
Cross-references: EMBL:U23472; NID:g775202; PID:g775203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pitle: Sequence analysis of the right end of Reference number: S59000; MUID:95304851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ap position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ene: SGD:ERRl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lesterhoeft, A.; Floeth, M.; Fritz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,346/Active site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tted to the Protein
                                                                                           Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         346/Active site: Glu, Lys #status
296,321/Binding site: magnesium 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            position: 15R
                                                                                                                                                                                                                                                                                       304 WSSWS 308
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                                                                                                                                                                                                                               13
                                                                                                                                                                                                                                                                                                                         1 WSXWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                references: EMBL:273637; MIPS:YPL281c; NID:g1370577; PID:e246987; PID:g1370578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the Protein Sequence Database, ce number: S67306
                                                                                                                                                                                                                                                                                                                                                             h 96.8%;
Similarity 80.0%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-437 <DUE>
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                                             Jackson-Grusby, L.L.; Ross, S.R.; ad. Sci. U.S.A. 89, 3864-3868, 199 intal-specific expression from the mber: A44090; MUID:92237269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e; gluconeogenesis;
(Ser) #status pred:
                                                                                                       L.L.; Ross, S.R.; Linzer, D.I.H
                                                                                                                                                                                                                                                                                                                                                             Score 30; DB 2;
Pred. No. 2.3e+02;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     tatus predicted predicted (Asp, Glu, Asp) #status predicted
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, May 1996
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                                                               mouse placental lactogen II gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycolysis; hydro-lyase;
                                                                                                                                                                                                                                                                                                                                                                                               Length 437
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RESULT 15
S14081
erythropoietin;
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232 WSAWS

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A; Molecule type: protein A; Residues: 32-50 <LIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A94049; MUID:85242683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-222 <SHI>
                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 268, 11208-11216, 19
Title: Functional erythropoletin
Reference number: A46713; MUID:93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Linzer, D.I.H.; Lee, S.J.; Ogren, roc. Natl. Acad. Sci. U.S.A. 82, 4;Tille: Identification of prolifer
                                                                                                                                                                                                                                                                                       Experimental source: PC12 and erythroid celinote: sequence extracted from NCBI backbone
                                                                                                                                                                                                                                                                                                                                                               Molecule type: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Rattu
Date: 21-Sep-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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Superfamily: prolactin
                                                                                                                                                                                                                                                                                                                             Cross-references: GB:D13566; NID:g286209;
                                                                                                               35-249/Domain: extracellular #status predi
25-238/Domain: cytckine receptor homology
550-271/Domain: transmembrane #status pred
772-507/Domain: intracellular #status predi
75/Binding site: carbohydrate (Asn) (coval
                                                                                                                                                                                                                                                         Keywords:
                                                                                                                                                                                                                                                                 Superfamily: erythropoletin receptor; cytokine receptor homology
                                                                                                                                                                                                                                                                                                                                                                                                       Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keywords: hormone; placenta
1-31/Domain: signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross references: GB:M14647; NID:g200404; PID:g200405
Linzer, D.I.H.; Lee, S.J.; Ogren, L.; Talamantes, F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title: Molecular cloning
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                                                    Local
1 WSXWS 5
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                                                                                                                                                                                                                               cytokine receptor; glycoprotein; transmemb
n: signal sequence #status predicted <SIG>
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                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           us norvegicus (Norway rat)
1993 #sequence_revision 18
                                  Conservative
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                                                                                                                                      transmembrane *status predicted <TMM>
intracellular *status predicted <INT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.; Takahata, K.; Konishi, Y.;
11208-11216, 1993
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ning of mouse p
                                               96.8%;
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                                                                                                                                                                                             #status predicted <EXT>
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                                               Score 30;
Pred. No.
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4356-4359, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30; DB 2;
Pred. No. 1.3e+02;
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                                Mismatches
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                                                                                                                                                                                                              #status predicted
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                                                                  В
                                                                                                                                                                                                                                                  transmembrane
                                                                                                                                                                                                                                                                                    (NCBIN:132811, NCBIP:132813)
                                                                                                                     #status
                                                                Length 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                  neural characteristics
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                          Gaps
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C. Species: Mus musculus (house mouse)
C. Stecies: Mus musculus (house mouse)
C. Accession: S14081; 14953
C. Accession: S14081; 14953
A. Title: Characterization of murine erythropoletin receptor genes.
A. Title: Characterization of murine erythropoletin receptor genes.
A. Reference number: S1249; MUID:91080149
A. Accession: S14081
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-265 KURP
A. Reference number: 149653; MUID:91201346
A. Referen
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Result

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Sequence

OM protein

9

Query Match Best Local S Matches 4 CKLEOX ALBR_KLEOX P10488; 44 CHAIN SEQUENCE 01-JUL-1989 (REL. 11, CREATED)
01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
01-JUL-1989 (REL. 11, LAST ANNOTATION UPDATE)
ALBICIDIN RESISTANCE PROTEIN.
KLEBSIELLA OXYTCCA.
BACTERIA, PROTEOBACTERIA; GAMMA SUBDIVISION; 1
KLEBSIELLA. This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for compatitude of the statement is not removed. ADRO_MOUSE STANDARD; PRT; 494 AA. 6051578; 15-JUL-1998 (REL. 36, CREATED) 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) NADPH:ADRENODOXIN OXIDOREDUCTASE PRECURSOR (ERECUCTASE) (FERREDOXIN-NADP(+) REDUCTASE). "CDNA cloning of mouse i BIOCHIM. BIOPHYS. ACTA 1 -1- CATALYTIC ACTIVITY: MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VER RODENTIA; SCIUROGNATHI; MURIDAE; EMBL; D49920; E212200; -. or send MEDLINE, 96085117. STRAIN-C57BL/6; EQUENCE FROM N.A. 11 WSAWS 1 WSXWS 5 PATHWAY: CHOLESTEROL SIDE-CHAIN-CLEAVAGE SYSTITISSUE SPECIFICITY: EXPRESSED IN THE ADRENAL, TO A LESSER EXTENT IN THE LIVER AND KIDEY'S SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX. ADRENODOXIN + NADPH.
COFACTOR: FAD FLAVOPROTEIN MGI:104724; FDXR.

DREDUCTASE; FLAVOPROTEIN; NADP; 29 Similarity 4; Conserv PEPTIDE. s requires a license agreement (S an email to license@isb-sib.ch). 15 35 494 AA; 93.5 93.5 STANDARD TISSUE-KIDNEY; 34 494 54202 CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; THI; MURIDAE; MURINAE; MUS. YAMADA E., 897 517 96.8%; ferredoxin reductase from kidney."; 1264:159-162(1995). REDUCED ADRENODOXIN + NADP(+) = OX ¥ CYRB_HUMAN <u>,</u> Score 30; Pred. No. MITOCHONDRION (POTENTIAL)
ADRENODOXIN REDUCTASE.
; 81A18E21 CRC32; PRT; YOSHIMURA T., TSUJIKAWA K., ALIGNMENTS Mismatches FAD; 218 DB 1; 1.7e+02; 1; (See http://www.isb-sib. MITOCHONDRION; (EC 1.18.1.2) (ADRENODOXIN ENTEROBACTERIACEAE; SYSTEM. ENAL, TESTIS Length 494; Indels P32927 Q20806 OXIDIZED AND a collaboration KOHAMA 0 OVARY homo sapien caenorhabdi outstation 0

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RESULT 3
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Best Local Similarity
Matches 4; Conser
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SEQUENCE FROM N.A.
STRAIN-JMP4505;
MEDLINE; 89013885.
WALKER M.J., BIRCH R.G., PEMBERTON J.P.
"Cloning and characterization of an a."
Klebsiella oxytoca."
7.447-484/1988)
                                                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (REL. 13, 0
01-AUG-1991 (REL. 19, 1
15-JUL-1998 (REL. 36, 1
COMPLEMENT COMPONENT CO
   CHAKRAVARTI
                SEQUENCE OF 1-491
MEDLINE; 89202413.
                                               MEDLINE; 93291175.
HOBART M.J., FERNIE B., DISCIPIO "Structure of the human C6 gene."
BIOCHEMISTRY 32:6198-6205(1993).
                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 89380223.
DISCIPIO R.G., HUGLI T.E.;
The molecular architecture of human
The molecular 264:16197-16206(1989).
                                                                                                                                                                                                                                 sixth
                                                                                                                                                                                                                   C5b-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     MEDLINE; 90036879
                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                               EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y00558; G43786; -. PIR; S02828; S02828.
ANTIBIOTIC RESISTANCE; PI SEQUENCE 218 AA; 25858
                                                                                                                                                                                                                                                                                                   PRIMATES; CATARRHINI;
                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                              CO6_HUMAN
                                                                                                                                                                                                                                        Complete primary structure and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: ALBICIDIN RESISTANCE PROTE WITHOUT ANTIBIOTIC ACTIVITY BUT WITH CHEMICAL MODIFICATIONS TO ALBICIDIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: ALBICIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WSXWS 5
                                                                                                                                                                                                                   component of the human complement inding domain in complement C6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MICROBIOL.
                                                                                                                                                                                                     ing domain in complement C6. CHEM. 264:18041-18051(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ); S02828.
RESISTANCE; PERIPLASMIC.
218 AA; 25858 MW; 87C032C5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                          N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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   CHAKRAVARTI
                           FROM
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9, LAST SEQUENCE UPI
6, LAST ANNOTATION (
T C6 PRECURSOR.
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                           N.A.
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                                                                                                                                                                                                                                   VIAL N., JENN
and functional
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Pred.
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                                                                      R.G.;
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  PARRA C.A.,
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albicidin
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*onal characterization
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 MUELLER-EBERHARD
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                                                                                                                                                                                                                            acterization of Identification
                                                                                                                                            component C6.";
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H.J.;
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DEWALD G., NOTHEN M.M., CILLUM.

POLlymorphism of human complement component C6: an amiliary component (C1) and complement component 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J05064; G179704;
EMBL; J05024; G307228;
EMBL; X72177; G825633;
EMBL; J04506; G618466;
PIR; A32109; A32109.
        DOMAIN
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TRANSMEM
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TRANSMEMBRANE.
SIGNAL
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural homology channel forming prote
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SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
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PS00022; EGF_1; 1.
PS01186; EGF_2; FALSE_NEG
PS01209; LDLRA_1; 1.
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A34372.
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; sushi; 2.
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I. U.S.A. 86:2799-2803(1989).
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                                                                                                                                                                                                                                                                                                                     C5B-BINDING DOMAIN.
2 X SUSHI (SCR) REPEATS
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SEQUENCE
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P10643;
                                                                                                                                                                                                                                                                                        use by non-profit institue modified and this statement
                                                                                                                                                                                                                                                                          entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., MEDLINE; 88087145. DISCIPIO R.G., CHAKE
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01-JUL-1989 (REL.
15-JUL-1998 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISCIPIO R.G., CHAKRAVARI D.N., MUELLER-EBERHARD H.J., Phe structure of human complement component C7 and the
                                                                                                                                                                                                                                                    tities requires a license agreement (send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOL. CHEM. 263:549-560(1988).
- FUNCTION: C7 IS A CONSTITUENT
                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: MONOMER OR DIMER; AS A C5B-7 COMPLEX IT CA FORM MULTIMERIC ROSETTES.

PYM: C7 HAS 28 DISCULFIDE BRIDGES.
SIMILARITY: TO COMPLEMENT FACTORS C6, C8, C9, AND TSIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
SIMILARITY: CONTAINS 2 TYPE-1 TSP REPEATS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
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                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It ween the Swiss Institute of Bioinf European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: C7 IS A CONSTITUENT OF THE MEMBRANE ATTACK COMPLEX C7 BINDS TO C5B FORMING THE C5B-7 COMPLEX, WHERE IT SERVES AS A MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAPIENS
; PS00279; MAC_PERFORIN; 1

; PS00022; EGF_1; 1.

;; PS01186; EGF_2; 1.

;; PS01209; LDLRA_1; 1.

;; PS50068; LDLRA_2; 1.

PF00057; Id1_recept_a; 1.

PF00057; Id1_recept_a; 1.

PF00090; tsp_1; 2.

PF00090; tsp_1; 2.
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4; Conservative
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9 (REL. 11, LAST SEQUENCE UP
8 (REL. 36, LAST ANNOTATION
COMPONENT C7 PRECURSOR.
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METAZOA; CHORDATA; VERTEBRATA;
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Pred. No. 3.1e
0; Mismatches
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Best Local S
Matches 4
MEDLINE: 95278905.

MICHELOTTI G.A., SNIDER J.V.,

"GENOTIC organization of huma
further examination of its 11.

HUM. GENET. 95:513-518(1995).

-i- FUNCTION: C8 IS A CONSTITUTE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CO8A_HUMAN STANDAI

P07357; Q13668;

O1-APR-1988 (REL. O7,

O1-FEB-1995 (REL. 31,

15-JUL-1998 (REL. 36,

COMPLEMENT COMPONENT C
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PLASMA; MEMBRANE ATT;
REPEAT; SUSHI; TRANS;
SIGNAL 1
                                                                                                                                                                                                                   "Complementary DNA and derived amino acid
subunit of human complement protein C8: e
a separate alpha subunit messenger RNA.";
BIOCHEMISTRY 26:3556-3564(1987).
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                                                                                                     TISSUE-BLOOD
                                                                                                                                                                                                                                                                                                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
PRIMATES; CATARRHINI; HOMINID
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                      SUBMITTED (FEB-1993)
                                                                                                                                                                                       REVISIONS TO 467-479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
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                                                                                                                                                                       J.M.
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                                                                    SNIDER J.V.,
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31, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
ENT C8 ALPHA CHAIN PRECURSOR
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EGF-LIKE.
TYPE-1 TSP:
2 X SUSHI (1)
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Pred. No. 2.
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AE; HOMO.
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2.8e+02;
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                                  beta
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HSSP; PO1130; ILDR.

COMPLEMENT PATHWAY; COMPLEMENT ALTI
COMPLEMENT PATHWAY; COMPLEX; C
PLASMA; MEMBRANE ATTACK COMPLEX; C
EGF-LIKE DOMAIN; REPEAT.

SIGNAL
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POTER
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COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M16974; G179718
EMBL; U08006; G901864
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EMBL; U07997; G901864;
EMBL; U07999; G901864;
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EMBL; U08003; G901864;
EMBL; U08004; G901864;
EMBL; U08004; G901864;
EMBL; U08004; G901864;
EMBL; U08005; G901864;
                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00279; MAC_PERFORIN; 1
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; FALSE_NE(
PROSITE; PS01209; LDLRA_1; 1.
PROSITE; PS50068; LDLRA_2; 1.
PFAN; PF00057; ldl_recept_a; 1.
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  545
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SUBUNIT: C8 IS COMPOSED OF THREE CHAINS: ALPHA, BETA AND GAMMA
THE ALPHA AND GAMMA CHAINS ARE DISULFIDE BONDED.
SIMILARITY: TO COMPLEMENT FACTORS C6, C7, C9, AND TO PERFORIN.
SIMILARITY: CONTAINS 1 TYDE-1 TSP REPEATS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
                         SMXSM
 SMSSM
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                                               h 96.8%;
Similarity 80.0%;
4; Conservative
549
                         u
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tsp_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s a license agreement
to license@isb-sib.ch
                                                                                                               575
65163
                                                                                                                   BY SIMILARITY.
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194 INTERCHAIN (WITH C8
POTENTIAL.
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Q -> K / T
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644 JOINED
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                                               Pred. No. 2e+(
0; Mismatches
                                                                                                                                                                                                                                                                               POTENTIAL.

COMPLEMENT COMPONENT C

TYPE-1 TSP 1.

LDL-RECEPTOR CLASS A.

POTENTIAL.
                                                                                                                                                                                                                                           POTENTIAL.
EGF-LIKE.
TYPE-1 TSP
                                                                                                              -> K (IN
-> S (IN
-33C94C53
                                                                                                                                                                                                                                                                                                                                                                       ALTERNATE PATHWAY; GLYCOPROTEIN;
K; CYTOLYSIS; SIGNAL; TRANSMEMBR?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORMING THE C5B-8 COMPLEX. C5-B8 T IN THE POLYMERIZATION OF C9. EE CHAINS: ALPHA, BETA AND GAMMA.
                                                           DB 1;
2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                              REF. 3).
REF. 3).
                                               ۳
                                                                                                                                                                                       C8-GAMMA).
                                                                      Length 584;
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                                                                                                                                                                                                                                                                                                                                                                       TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                    ALPHA CHAIN
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PROSITE; PS011
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsithe European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and sequencing of complement component C9 and its 1
DOC-2 in the pufferfish Fugu rubripes.";
GENE 200:203-211(1997).
-1- FUNCTION: C9 IS THE FINAL COMPONENT OF THE COMPLEMENT SY
ADDED IN THE ASSEMBLY OF THE MEMBRANE ATTACK COMPLEX. IT
TO ENTER LIPID BILAYERS, FORMING TRANSMEMBRANE CHANNELS
                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as lon modified and this statement is not removentitles requires a license agreement (s or send an email to license@isb-sib.ch).
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
COMPLEMENT COMPONENT C9 PRECURSOR.
                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                             PROSITE; PS50068;
PFAM; PF00057; 1d
HSSP; P01130; 1AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII;
TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA;
TETRAODONTIFORMES; TETRAODONTOIDEI; TETRAODONTIDAE; FUGU.
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           Similarity
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                                                                                                                                                                                                                                                                                                         PS00279; MAC_PERFORIN; 1.
PS00022; EGF_1; 1.
PS01186; EGF_2; FALSE_NEG
PS011209; LDLRA_1; 1.
                                                     ELGAR G.,
                                                                                                                                                                                                                                                                                                                                                       G1845349;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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ng of complement component
sh Fugu rubripes.";
         .08;
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Score 30; DB 1;
Pred. No. 2e+02;
0; Mismatches
                                                                                                                                                                                          COMPLEMENT COMPONENT OF TYPE-1 TSP 1.
LDL-RECEPTOR CLASS A.
EGF-LIKE.
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BY SIMILAR
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40CEB614
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                                                                                                                                                                                                                                                       ALTERNATE PATHWAY; GLYCOPROTEIN; X; CYTOLYSIS; SIGNAL; EGF-LIKE DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               586
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                                                     CRC32
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8,
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01-AUG-1992 (REL. 01-AUG-1992 (REL. 01-NOV-1997 (REL.

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CREATED)
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LAST ANN

ANNOTATION SEQUENCE

ON UPDATE)

BETA CRYSTALLIN

CRBB_BOVIN BOVIN

STANDARD;

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Query Match
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Matches 4
                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARIT DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR VERY SIMILAR GREEK KEY MOTIFS.
                                                                                                                                                                                                                                                                                                                                                                                                                entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                  NIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                              nodified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Homology between the primary structures of crystallin chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 84132067.
BERBERS G.A.M., HOEKMAN W.A.,
KLEINSCHMIDT T., BRAUNITZER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; I
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 91340151.
VAN RENS G.L., DRIESSEN H.P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRYBA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILOEMENDAL H.:
Isolation and characterization of cDNAs encoding beta A2- and beta
44-crystallins: heterologous interactions in the predicted beta
44-beta B2 heterodimer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISSUE-LENS CORTEX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE OF 133-196.
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                                                                                                                                                                                                                                                                                                                                                                                             send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       LENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CRYSTALLINS ARE TO
OF THE VERTEBRATE EYE LENS.
   Similarity
4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                requires a license agreement
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 Conservative
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139:467-479(1984).
139:467-479 ARE THE DOMINANT
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                  96.8%;
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CONNECTING PEPTIDE.
MOTIF 3.
MOTIF 4.
                  Pred. No. 73;
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N-TERMINAL AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOEMENDAL H.,
                                                                                    NH -> HAQ (IN REF. 9867FFC9 CRC32;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NALINI V., SLINGSBY C.,
                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions
                                                                                                                                                                                                                ARM
                                   DB 1;
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1; Indels
                                   Length 196;
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E; BOVINAE;
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Matches 4
SEQUENCE FROM N.A. MEDLINE; 90304340.
JONES S.S., D'ANDRI
                                                "The erythropoletin receptor ge multiple transcripts in an eryt EXP. HEMATOL. 19:973-977(1991).
                                                                                                                         HOMO SAPIENS (HUMAN).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                        01-NOV-1990
01-NOV-1990
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                       MEDLINE; 91372359.
EHRENMAN K., ST JOHN T.;
                                                                                                     SEQUENCE FROM N.A. MEDLINE; 91372359.
                                                                                                                                                                                                                                                                         MAMDH
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSFERASE;
SIGNAL
                                                                                                                                                                                           ERYTHROPOIETIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED (JUL-1995)
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STRAIN-T-3040;
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P94286;
                                                                                                                                                                                                                                                                                                                          832 WSTWS 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GUMA T., KUROKAWA T., TOBE K., KOBAYASHI M.;
UBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

1- FUNCTION: PRODUCES CYCLOISOWALTOOLIGOSACCHARIDE FROM DEXTRAN

1- SIMILARITY: BELONGS TO FAMILY 66 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                              1 WSXWS 5
                                                                                                                                                                                                                                                           OR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5-TUL-1998 (REL. 36, CREATED)
5-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
5-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
YCLOISOMALTOOLIGOSACCHARIDE GLUCANOTRANSFERASE
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(REL. 16, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)
TIN RECEPTOR PRECURSOR (EPO-R).
                                                                                                                                                                                                                                                                                                                                                                           Conservative
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972
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                                                            or gene: cloning and erythroid cell line
                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 1; L
Pred. No. 3.3e+02;
0; Mismatches 1;
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CYCLOISOMALTOOLIGOSACCHARIDE
GLUCANOTRANSFERASE.
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                                                            identification
OCIM1.";
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L.L.,

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EMBL; M34986; G182201;
EMBL; M60459; G182245;
EMBL; S45332; G255497;
EMBL; M76595; G553281;
EMBL; M77244; G182134;
RECEPTOR;
SIGNAL
                                                                                                                                                                                                                                                                                                                or send an
                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human erythropoietin characterization."; BLOOD 76:31-35(1990).
                                                                                                                                                                                                                                                                                                                                 entities requires a
                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "An antagonist peptide-EPO receptor complex suggests "An antagonist peptide-EPO receptor complex suggests";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-17 FROM N.A. MEDLINE; 92147143. PENNY L.A., FORGET B.G.;
                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRETIEN S.;
(Cloning of the gene encoding)
(Cloning of the gene encoding)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOGUCHI C.T., BAE K.S., HANKINS W.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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ENOMICS 11:974-980(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDLINE; 92399734
AOUCHE L., TOURN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVNAH O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCT. BIOL. 5:993-1004(1998).

FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN MECHANISM OF ERYTHROPOIETIN INDUCED ERYTHROBLAST PROLIFE AND DIFFERENTIATION.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ing of the human erythropoietin receptor gene.";
78:2548-2556(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIU K.D., GOLDSMITH M.A.,
                                                PS00241; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99023198
             TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL;
                                                                                                         29-JUL-97
18-NOV-98
                                                                                                                                                                                                                                                                                                                  email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOHNSON D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOURNAMILLE C.,
                                                                                                                                                                               A43799.
                                                                                                                                                                                                                                                                                                            license@isb-sib.
                                                                                                                                                                                                                                                                                                                                                                  institutions as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor: cloning,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSON D.L., MIDDLETON S.A., JOLLIFFE L.K., WILSON I.A rotein hormone by a peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HATTAB C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HE W., KRAUSE C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human erythropoietin
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                                                   نزمر
                                                                                                                                                                                                                                                                                                                                                                                     There are no
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                                                                                                                                                                                                                                                                                                                                                                  as its content
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               3D-STRUCTURE
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Best Local
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P14753; Q638
01-APR-1990
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DISULFID
CARBOHYD
SEQUENCE
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DOMAIN
MUTAGENESIS.
MEDLINE; 93180826.
MIURA O., CLEVELAND
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 92017832.
HINO M., TOJO A., MISAWA Y., MORII H., TAKAKU
"Unregulated expression of the erythropoietin
insertion of spleen focus-forming virus long t
murine erythroleukemia cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
ATTERCHARMI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (REL. 14,
01-APR-1990 (REL. 14,
01-NOV-1995 (REL. 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 91080149.

KURAMOCHI S., IKAWA Y., TODOKORO K.;

"Characterization of murine erythropoletin receptor J. MOL. BIOL. 216:567-575(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                           LACOMBE C., CHRETIEN S., LEMARCHANDEL V., GISSELBRECHT S., CARTRON J.P.;
                                                                                                                                                                             MEDLINE; 91201346
                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-27 F
MEDLINE; 90287158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 89195238.
D'ANDREA A.D., LODISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
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                                                                      riend leukemia
7. BIOL. CHEM. 2
                                                                                                                                                                                                                                                                      Structure and
                                                                                                                                                                                                                                                                                       COUSSOUFIAN H.,
                                                                                       ctivation of the murine erythropoletin riend leukemia cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 WSAWS 237
                                                                                                                           Spleen focus-forming virus long
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                                                                                                                                                                                                                                 BIOL. 10:3675-3682(1990)
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                                                                    266:6952-6956(1991)
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LAST ANNOTATION UPDATE)
OR PRECURSOR (EPO-R).
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A567A994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 1;
Pred. No. 1.8e+02
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EXTRACELLULAR (
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                                                                                                                           terminal repeat
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                                                                                                                                                              MAYEUX
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MUS.
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Q07303;
01-FEB-1995
01-FEB-1995
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DISULFID
DISULFID
                                                                  RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PS00241; RECEPTOR_CYTOKINES_1;
PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
PFAM; PF0041; fn3; 1.
HSSP; P19235; 1EBP.
               MASUDA S.,
                                                                                                                        ERYTHROPOIETIN
                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institu modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Inactivation of erythropoletin receptor function by point mutations in a region having homology with other cytokine receptors."; MOL. CELL. BIOL. 13:1788-1795(1993).

-i- FUNCTION: RECEPTOR FOR ERYTHROPOLETIN. MAY PLAY A ROLE IN THE
                                   EQUENCE FROM N.A. EDLINE; 93266574.
                                                                                                                                                                                                                                          232 WSAWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch
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                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                1 WSXWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. SIMILARITY: CONTAINS I FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND DIFFERENTIATION
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                                                                                                                                                                                                                                                                                                 Similarity
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               NAGAO M.,
SASAKI R.,
                                                                                                                                                                                                                                          236
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  erythropoietin receptor of the
                                                                                                               (REL. 31, CREATED)
(REL. 31, LAST SEQUENCE UPDATE)
(REL. 31, LAST ANNOTATION UPDATE)
FIN RECEPTOR PRECURSOR (EPO-R).
                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                291
55194
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                       TAKAHATA K., KONISHI Y.,
                                                                                                                                                                                                                                                                                                 96.8%;
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BY SIMILARITY.
POTENTIAL.
E -> D (IN E909)
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Pred. No. 1.8e+02;
0; Mismatches 1
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CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
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C90C07B8 CRC32;
                                                                                                                                                                              507
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cells with neural
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                       GALLYAS
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Best Local S
Matches 4
                                                                                                                     SEQUENCE FROM N.A. STRAIN-S288C / AB972; CHURCHER C.M., LOUIS SUBMITTED (NOV-1995)
       PRYDE F.E., HUCKLE T.C., LOUIS E.J.;
"Sequence analysis of the right end of chromosome cerevisiae: an insight into the structural and fun significance of sub-telomeric repeat sequences.";
YEAST 11:371-382(1995).
                                                                                                                                                                                                ENOLASE RELATED PROTEIN 1 (EC 4.2.1.11).
ERRI OR YMR323W OR YM9924.15.
SACCHAROMYCES CERVUISIAE (BAKER'S YEAST)
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMY
                                                                                                                                                                                                                                                     P42222;
01-NOV-1995
01-OCT-1996
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                      YEAST
                                                                    MEDLINE; 95304851
                                                                                               SEQUENCE OF 120-437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                     SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                       ERR1_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          characteristics. Comparison
                                                                                                                                                                                                                                                                                                                                                                    232 WSAWS 236
                                                                                                                                                                                                                                                                                                                                                                                        1 WSXWS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOL. CHEM. 268:11208-11216(1993).
FUNCTION: RECEPTOR FOR ERVIHROPOIETIN. MAY PLAY A
MECHANISM OF ERVIHROPOIETIN-INDUCED ERVIHROBLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00340; RECEPTOR_CYTOKINES_1; 1. PS00340; RECEPTOR_CYTOKINES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                             (REL. 32, CREATED)
(REL. 34, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   507 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                               / AB972;
                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                              FROM N.A.
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                                                                                                                     I., BARRELL B.G., I
EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.
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POTENTIAL.
MW; 5C20ECC3 CRC32;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
ENTHROPOIETIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                RAJANDREAM M.A.,
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                                                                                                                     DATA
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Best Local S
Matches 4
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P15509; Q14429;
01-APR-1990 (REI
                                             SEQUENCE OF 1-385 FROM N.A.

MEDLINE; 94193800.

NAKAGAWA Y., KOSUGI H., MIYAJIMA A., ARAI

"Structure of the gene encoding the alpha
granulocyte-macrophage colony stimulating
Implications for the evolution of the cyto
                                                                                                                                                                                                                                                        HUX., EMANUEL P.D., ZUCKERMAN K.S.;

"Cloning and sequencing of the cDNAs encoding t
splicing-derived variants of the alpha subunit
granulocyte-macrophage colony-stimulating facto
BIOCHIM. BIOPHYS. ACTA 1223:306-308(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR
CHAIN PRECURSOR (GM-CSF-R-ALPHA) (CDW116) (CD116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 90059966.
GEARING D.P., KING J.A., GOUGH N.M.
"Expression cloning of a receptor colony-stimulating factor.";
EMBO J. 8:3667-3676(1989).
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 94368898.
HU X., EMANUEL P.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAGOA; CHORDATA; VERTEBRATA; MANMALIA;
PROTMATES: CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSF2RA OR CSF2R
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.
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ISSUE-PLACENTA;
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SIMILARITY: BELONGS
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; U23472; G775203; -
. L0002735; ERR1.
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269:10905-10912(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GM-CSF-R-ALPHA-1).
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r human granulocyte-macrophage
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                                                                           I K.I., YOKOTA T.;
a subunit of the hu
g factor receptor.
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                                                                                                                                                                                                                                                                                          factor receptor.";
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QY.

1 WSXWS 5

Query Match Best Local S Matches 4

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DB 1; 1.4e+02;

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FACTOR.
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RECEPTOR_CYTOKINES_2;
MBRANE; GLYCOPROTEIN;
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                       INVSGDLENRYNFPSS -> VVLTTGTSALCTFMCS (IN GM-CSF-R-ALPHA-2), MISSING (IN GM-CSF-R-ALPHA-2). GSDDGNLGSVIIYVLLIVGTLVCGIVLGFLFKRFLRIQRLF PPVPQINDKLNNHEVEDEIIMEEFTPEEGKGYREEVLTVK EIT -> DDHLGGIHPRGRERLPRRGLDREGNYLRPRGCRN GMDISSATRGNCFLDDAVNLYIIFYVFI (IN GM-CSF-
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PROSITE; PS00128; LACTALBUMIN_LYSOZYME;
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EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
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FUNCTION: UNLIKELY TO PLAY AN AND CEPTENSE. MAY UNITED PROPERTY.
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TISSUE SPECIFICITY: FOUND IN THE MIDGUT
DEVELOPMENTAL STAGE: MAXIMAL EXPRESSION IS FOUND DURING THE THIRD LARVAL INSTAR, IT DROPS TO BECOME UNDETECTABLE IN THE LATE PUPAL STAGE: THE EXPRESSION IN ADULTS IS SIMILAR TO THAT OF FIRST AND
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European Bioinformatics Institute.
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PIR; S32643; S32643.
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DAFFRE S., XYLSTEN P., SAMAKOVLIS C., HULTMARK D.;
The lysozyme locus in Drosophila melanogaster: an ex
family adapted for expression in the digestive tract.
MOL. GEN. GENET. 242:152-162(1994).
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TISSUE SPECIFICITY: FOUND IN THE MIDGUT.

LARVAL STAGE: MAXIMAL EXPRESSION IS FOUND DURING THE THIRLIPPOLYMENTAL STAGE: MAXIMAL EXPRESSION IS FOUND THAT OF FIRST AND STAGE. THE EXPRESSION IN ADULTS IS SIMILAR TO THAT OF FIRST AND
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Search completed: September 17, 1999, 03:10:11 Job time: 291 sec

GenCore version 4.5 (c) 1993 - 1998 Comp Compugen Ltd.

OM protein protein search, using sw model

Run on: September 17, 1999, 03:08:10; Search time 64.1 Seconds

152.611 Million cell updates/sec

Perfect score: US-09-037-657-13

Scoring table: BLOSUM62 MPAGRPGPVAQSARRPPRPL......WRAWMQKSHKTRNQVLPAKL 413

Searched: 188963 seqs, 23686106 residues

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score d being printed,

SUMMARIES

Result No.

Query Match
Best Local Similarity
Matches 413; Conserv

Conservative

Score 2251; DB 1; Pred. No. 5.4e-186; Mismatches

Indels Length

Gaps

0

413; 0,

R11742 R14255

Clone Human recepto

ALIGNMENTS

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The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis,
                              and survival. The pe.g. for cancers or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel haemopoietin receptor NR6.1 protein.
Haemopoietin receptor; cell proliferation; cell differentiation; cancer;
cell survival; therapeutic; neuronal proliferation; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -PSDB; V27140.
New isolated haemopoletin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Kojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
Dang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W55011 standard; Protein; 413 AA.
                                                                                                                                                                                                                                                                                                                                                                 .g. neuronal c
laim 14; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DZIE/) DZIEGLEWSKA H E.
413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               nemopoletin receptor - used for developing products proliferation, differentiation and survival of cells,
                                                                                                                                                                                                                                                                                                                                                         77-81; 182pp; English.
                          ន
                       cancers,
                   or for drug screening.
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	361 PSSGPVRRELKOFLGWLKKHAYCSNLSFRLYDOWDAWNOKSHKTBNOVI DAVI 413	ğ
360	301 LAGLKPGTVTFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE	皮
360		Qy
300	241 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR	문
300	~	. Q
240	181 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDD	뭥
240		Ϋ́
180 -	121 ARDSSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW 180	F
180		δ.
120		당
120	61 ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH	Ş
60	1 MPAGRPGPVAQSARRPPRPLSSLMSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ 60	문
60	1 MPAGRPGPVAQSARRPPRDLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ	Q

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361

W55012

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The haemopoietin receptor (HR) NR5.2 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening. Sequence 425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated haemopoletin rece
for modulating proliferation,
e.g. neuronal cells
Claim 15; Page 84-87; 182pp; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel haemopoietin receptor Haemopoietin receptor; cell cell survival; therapeutic;
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMKAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
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                            PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS 414
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sh A, Nicola NA, 1
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proliferation; cell dif
neuronal proliferation;
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Pred. No. 7.2e-184;
2; Mismatches 0;
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ID W5990

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This is the amino acid sequence of the murine U4 protein from the CC This is the amino acid sequence of the murine U4 protein from the CC This is the modulation of cell proliferation, or the immune cc invention for the modulation of cell proliferation, or the immune cc used to produce recombinant CC Invention for The U4 protein is used to screen for specific binding cgents, raise antibodies. It is also used as reagents for assays and capants, raise antibodies. It is also used as reagents for assays and compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune CC cented) thereived or the result of infection, autoimmune diseases, concer, and allergy).
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Best Local S
Matches 408
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15-JAN-1998; U00334
16-JAN-1997; US-784
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Murine; U4 protein;
cell proliferation;
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llarity 98.6%;
Conservative 2
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of the murine U4
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response; antibody; cell diff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2222.5; DB 1
Pred. No. 1.6e-183;
2; Mismatches 1;
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Query Match Best Local Matches

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Query Match
Best Local S
Matches 404
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Zcytor5; cytokinin-like receptor; d
maintenance factor; thyroid; heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mammalian cytokinin-like down-regulating Zcytor5 natur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 75-76;
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N-PSDB; V70896.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRÓOSGDNLVCH
                                                                                                                                  LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE
                                                                                                                                                                                                    PPDVHVSRVGGLEDQLSVRWVSPPALKDELFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                             LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE
                                                                                                                                                                                 PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Presnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 97.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZYMOGENETICS INC.
L, Foster DC, Gilbert
Presnell SR, Whitmore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heart enlargement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2197.5;
Pred. No. 2.3e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor Zcytor5 - useful for, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jelmberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2197.5; DB 1
No. 2.3e-181;
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cardiotrophin-1;
                                       414
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W7.0861 standard;

Protein;

425

417

RREVLPDKL 425

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Query Match
Best Local
Matches 39
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05-NOV-1998.
01-MAY-1998; US-074721.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-055030.
13-FEB-1998; US-053890.
13-FEB-1998; US-053890.
(AYMO) 2XMOGENETICS INC.
Adams RL, FOSTET DC, Gilbert T Lok S, Presnell SK, Whitmore T WFI; 99-034662/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 71-72; 55pp; English.

The present sequence represents an allelic varaint of protein designated Ecytor5, which is a cytckinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.

Sequence 425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W70861;
17-MAR-1999 (first
Allelic varaint of )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sap
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                                                                                                     PPDVHYSRVGGLEDQLSVRWYSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                               ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALALNLNGSROOSGDNLVCH
                                                        PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ
                                                                                                                                                                            PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                                                                                                                                                                                                                              ATCSVHGDPPGATAEGLYWTLNGRRLPPELSRYLNASTLALALANLNGSRQRSGDNLVCH
---VLPAKL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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91.1%;
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Pred. No. 8.4e
5; Mismatches
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ligands or de
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t; skeletal muscle;
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3.4e-173;
hes 13;
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Best Local Similarity
Matches 387; Conser
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13-FEB-1998; US-074771.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            down-regulating Cytor5 natural ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Zcytor5 protein sequence.
Zcytor5; cytokinin-like receptor; down-regulamaintenance factor; thyroid; heart; skeletal cardiac pathology; heart enlargement; Zcytor;
                                                                                                                                                                                                                                                          121
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N-PSDB; V70894.
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PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ----VLPA
                                                                                                         PPEVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                           PPDVHYSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
                                                                                                                                                                                YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
                                                                                                                                                                                                                                      ARDGSILAGSCLYVGLPPEKPENISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW
                                                                                                                                                                                                                                                                            ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH
                                                                                                                                                                                                                                                                                                                                  MPAGRRGPAAQSARRPP-PLLPLL--LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLL
                                                                                                                                                                                                                                                                                                                                                   MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ
                                                                     LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE
                                                                                                                                                                 YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDP
                                                                                                                                                                                                                        ARDGSILAGSCLYVGLPPEKPVNISCWSKNMXDLTCRWTPGAHGETFLHTNYSLKYKLRW
                                                    LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGE
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                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          92.9%;
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Pred. No. 2.7e-172;
8; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or5 - useful for, e.g.
detecting cardiotrophin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       muscle;
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New nucleic acid encoding U4 haematopoletin receptor superfamily PT Chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto: immune disease PS Claim 9; Pagees 29-30; 38pp; English.

CC This is the amino acid sequence of the human U4 protein from the haematopoletin receptor superfamily, used in the method of the CC Invention for the modulation of cell proliferation, or the immune CC response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding CC agents, raise antibodies. It is also used as reagents for assays and CC as tissue markers for isolation of cognate ligands and receptors, and cell differentiation, and the immune system (e.g. for treating immune CC deficiency, inherited or the result of infection, autoimmune diseases, Sequence 408 AA;
                                                                                                                                                                                                                                                                                                                                                  23-JUL-1998.
15-JAN-1998;
16-JAN-1997;
                                                                                                                                                                                                                                                                                                (GEMY) GENETICS INST INC.
Collins M. Donaldson DD, Neben
WPI; 98-414109/35.
                                                                                                                                                                                                                                                                                     N-PSDB; V41689
                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; U4 protein; haematopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of the human U4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W59805 standard; Protein; W59805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferation;
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; US-784863.
                                                                                                                                                                                                                                                                                                                                                                                                                                        immune response; antibody;
cancer; allergy.
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ody; cell differentiation;
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les 376; Conserv
GWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS
             GWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ----VLPA
                                                                                       QLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQV
                                           RCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFL
                                                       RCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGGVCEPRGGEPSSGPVRRELKQFL
                                                                                                    QLSVRWVSPPALKDELFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQV
                                                                                                                                    PHSCHIPKDLALFTPYEIWYEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLED
                                                                                                                                                PHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLED
                                                                                                                                                                                GLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVG
                                                                                                                                                                                               GLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVG
                                                                                                                                                                                                                                          EGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQOSGDNLYCHARDGSILAGSCLYV
                                                                                                                                                                                                                               EGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYV
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                      90.4%;
                                                                                                                                                                                                                                                                                                                         Score 2036; DB 1;
Pred. No. 1.7e-167;
7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                              Length
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RESULT W70841 ID W7

W70841

standard;

Human Zcytor5

cytokinin-like receptor; nce factor; thyroid; heart

down-regulation;

growth factor; cardiotrophin-1;

heart

17-MAR-1999

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Best Local S
Matches 368
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The present sequence represents a Zcytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
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Adams RL, Foster DC, Gilbert Lok S, Presnell SR, Whitmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-1
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01-MAY-1997;
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17-MAR-1999
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                                                                                                                                                                                                                                                                                    LALANINGSRQQSGDNIVCHARDGSILAGSCLYVGIPPEKPFNISCWSRNMKDLTCRWTP 160
                                                                                                          VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS 340
                                                                                                                                                                                                                                            GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL
                                                                                                                                                                                                                                                                                                                                                                  AHTAVISPODPTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLA 100
                  SHKTRNQ---VLPA 411
                                                         TPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWL
                                                                  TPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK
                                                                                                                                                                   GSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR
                                                                                                                                                                                  GSARSDYLTLDYVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR
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SHKTRNQDEGILPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 AA;
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US-045287.
US-850030.
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374
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Pred. No. 5.5e-165;
2; Mismatches 1;
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5 ligand; variant.
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W70840 standard; W70840;

Protein;

RESULT W70839 ID W7 AC W7 DT 17

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W70839 standard; Protein; W70839; 17-MAR-1999 (first entry)

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The present sequence represents a Zcytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered a down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effects of a growth and or example to lessen the effects of a growth and or example to lessen the effects of a growth and or example to lessen the effects of a growth and or example to lessen the effects of a growth and or example to lessen the effects of a growth and or example to lessen the effects of a growth and or example to lessen the effects of a growth and or example to lessen the effects of a growth and or example to lessen the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maintenance factor in the effects of a growth and or maint
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Lok S, Pre
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13-FEB-1998; US-07472
01-MAY-1997; US-04528
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RL, Foster DC, Gilbert
Presnell SR, Whitmore
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nilarity 92.9%;
Conservative
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Pred. No. 7.3e-163;
5; Mismatches 7;
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cting cardiotrophin-1
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Sequence 388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human 2cytor5 variant.

Zcytor5; cytokinin-like receptor; down-regulation; maintenance factor; thyroid; heart; skeletal muscle cardiac pathology; heart enlargement; 2cytor5 ligat
  W70850 standard;
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01-MAY-1997; US-045287
01-MAY-1997; US-850030
13-FEB-1998; US-023890
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New mammalian cytokinin-like redown-regulating Zcytor5 natural
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                                                           MQKSHKTRNQDEGILPS
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L, Foster DC, Gilbert
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 Protein;
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13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
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WPI; 99-034662/03.
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SHKTRNOHRTRGSCPRADGARREVLPDKL 389
                                                      TPRSERPGPGGGACEPRGGEPSSGPYRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK
                                                                                                                                                                                                                                                                                         LALANINGSRORSGDNIVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTP
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92.5%;
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Pred. No. 2.1e-161;
6; Mismatches 7;
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t; skeletal muscle; cardiotrophin-1;
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ds or detecting cardiotrophin-1
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Best Local Similarity 92.5%;
Matches 360; Conservative
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The present sequence represents a Zcytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and to anti-idiotypic antibody could be used to purify Zcytor5 and therappeutically to modify Zcytor5 ligand effects.
               Human
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Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
WPI; 99-034662/03
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ance factor; thyroid; heart
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ting cardiotrophin-1
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Claim 1; Page 89-90; 55pp; English.

CC The present sequence represents a Zcytor5 variant protein. Zcytor5

CC is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in CC thyroid, heart, and skeletal muscle for example to lessen the effect CC of cardiotrophin-l on cardiac pathologies, so preventing heart CC enlargement. Zcytor5 could be used to detect cardiotrophin-l in the CC comprising Zcytor5 DNA or RNA can be used to determine the prose CC comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the CC and integrity of antibody could be used to purify Zcytor5 and the CC therapeutically to modify Zcytor5 ligand effects.
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01-MAY-1998; US-074721.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
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Adams RL,
Lok S, Pr
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SHKTRNQHRTRGSCPRADGARREVLPDKL
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RL, Foster DC, Gilbert
Presnell SR, Whitmore
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Pred. No. 3.1e-161;
6; Mismatches 7;
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ALIGNMENTS

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                                                                                                                                                                                                                                                             Hypothetical protein SEQUENCE 2529 AA;
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YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A.,
SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M.,
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea;
                                                                                                                                                                                                                                                                                                            Nature 388:539-547(1997).
EMBL; AE000602; AAD07969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-26695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori (Campylobacter pylori).
Bacteria, Proteobacteria; epsilon subdivision;
Helicobacter
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01-JAN-1998 (TrEMBLrel. 05,
01-NOV-1998 (TrEMBLrel. 08,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
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ICE 367 AA;
                                                                                                                                                                        Similarity 80.
4; Conservative
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Last annotation updat
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1.9e+03;
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                                                                                                                                                                                                     Length 2529;
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Query Match
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Matches 4
                                                     *Molecular cloning of new x Submitted (CCT-1996) to the EMBL; D88553; BAA13641.1; Aylan degradation; Hydrolas SEQUENCE 528 AA; 58533 M
                                                                                                                                                                                                                                                            P70733
P70733;
                                                                                                                KAMIO Y
                                                                                                                       OKAI N., NGUYEN D.V., NARAYAN R.,
                                                                                                                                    STRAIN-W-6
                                                                                                                                              SEQUENCE FROM N.
                                                                                                                                                                                                                            01-FEB-1997
01-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z98268; CAB10963.
PFAM; PF00823; PPE; 1.
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01-JAN-1998 (TrEMBLrel. 05, C
01-JAN-1998 (TrEMBLrel. 05, L
01-NOV-1998 (TrEMBLrel. 08, L
HYPOTHETICAL 39.8 KD PROTEIN.
                                                                                                                                                                               Bacteria;
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PHILIPP W.J., POULET
BALASUBRAMANIAN V., )
                                                                                                                                                                     Aeromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protes
SEQUENCE 394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "An integrated Mycobacterium
                                                                                                                                                                                            \eromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-H37RV;
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Submitted
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                                                                                                                                                                                                                                                                                                                                                                         Similarity 80.
4; Conservative
                                                                                                                                                                              caviae.
Proteobacteria;
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(AUG-1997)
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                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                      Hydrolase;
58533 MW;
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              96.8%;
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                                                                                      the
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B., BERGH S.,
                                                                                      xylanase from Aeromonas
ne EMBL/GenBank/DDBJ data
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s H37Rv, a
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EMBL/GenBank/DDBJ
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Last sequence update)
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           Score
Pred.
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Pred. No. 3
                                                     Glycosidase.
8D84F6AD CRC32;
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           NO;
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           DB 2;
4.6e+02;
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BLOOM B.R., JP
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3.5e+02;
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on update)
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                      Length 528;
                                                                                                                       KANEKO J.,
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with Myco
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                                                                                                                                                                            group;
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Best Local :
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01-MAY-1999 (TREMBLIE
01-MAY-1999 (TREMBLIE
PUTATIVE VACUOLATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gastric Pathogen Helicobacter Nature 397:176-180(1999).
EMBL; AE001515; AAD06432.1;
                                                                                                                                                                                  Submitted (JUL-1996) to the EMBL/GenBank/DDBJ
EMBL; 274814; CAA99082.1; -.
SEQUENCE 455 AA; 52678 MW; 15DC3CC3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation updat
CHROMOSOME XY READING FRAME ORF YOLD YOUR CHROMOSOME XY READING FRAME ORF YOLD YOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALM R.A., LING L.-S.L., N
SMITH D.R., NOONAN B., GU
TUMMINO P.J., CARUSO A.,
GIBSON R., MERBERG D., M.
                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker
Eukaryota; Fungi; Ascomycota; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q08231
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                                                                                                                                                                                                                                                                          EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic Sequence Comparison of Two Unrelated astric Pathogen Helicobacter pylori.";
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                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.

LEXANDRAKI D., KATSOULOU C., TZERMIA M.;

LEXANDRAKI D., KATSOULOU C., TZERMIA M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lelicobacter.
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78
                                                                                                                                                                                                                                                                                                                                                                                                     ccharomycetaceae;
                                       1 WSXWS
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WSAWS
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                                                                                   Similarity
4; Conserv
82
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(Tremblrel 10, Last seq
(Tremblrel 10, Last ann
CUOLATING CYTOTOXIN (VACA
                                                                                   Conservative
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AA; 260015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   Ascomycota; Hem
e; Saccharomyces
                                                                                                     96.8%;
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GUILD B.C., DEJONGE B.L., CARMEL G
URLA-NICKELSEN M., MILLS D.M., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MILLS
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                                                                             Score 30; DB
Pred. No. 4e+0
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                                                                                                                                                                                    15DC3CC3 CRC32;
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st annotation update)
(VACA) PARALOG.
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1.8e+03;
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4e+02;
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Best Local S
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                            SEQUENCE FROM N.A.
ANDREWS S., HOLMES A
Submitted (FEB-1998)
                                                                                                               01-JUN-1998 (TremBLrel.
01-JUN-1998 (TremBLrel.
01-MAY-1999 (TremBLrel.
                                                                                                                                                                                                                                                                                                        ACT_SITE
METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: GLYCOLYSIS.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
EMBL; Z75301; CAA99775.1; -.
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DUESTERHOEFT A., FLOETH M., FRITZ M., HILBERT SUBMITTED (JUN-1996) to the EMBL/GenBank/DDBJ-1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
DELIUS H., HEBLING U.;
Submitted (JUN-1996) t
         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE)
                                                                         Eutheria;
                                                                                             Homo sapiens (Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-331 FROM N.A.
DELIUS H., HEBLING U., HOFMANN B.
Submitted (JUL-1996) to the EMBL/
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JUN-1998 (TrEMBLrel 06, Last seq
MAY-1999 (TrEMBLrel 10, Last ann
CLONE GS164B05 FROM 7P21-P22, CC
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COFACTOR: MAGNESIUM IS REQUIRED FOR
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                                                                                  Metazoa;
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                                                                                                                                                          PRELIMINARY;
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                                                                       Chordata; Cr
Catarrhini;
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0; Mismatches
                              EMBL/GenBank/DDBJ databases.
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MAGNESIUM (BY S
W; 1E54CA23 CRC3
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                                                                                  Craniata;
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                                                                        Hominidae;
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, COMPLETE SEQUENCE
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3.9e+02
                                                                                Vertebrata;
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databases.
- PHOSPHOENOLPYRUVATE
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NON_TER
SEQUENCE
                                       RAINES M.A., LIU L., QUAN S.G., JOE V., DIPERSIO J.F., GOLDE "Identification and molecular cloning of a soluble human granulocyte-macrophage colony-stimulating factor receptor."; Proc. Natl. Acad. Sci. U.S.A. 88:8203-8207(1991).
                                                                                                                            01-NOV-1996 (TremBlrel. 01.
01-NOV-1998 (TremBlrel. 08
GM-CSF RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                     Transmembrane.
SEQUENCE 410
                 FISSUE-PLACENTA,
                         SEQUENCE FROM N.A.
                                                                                                       Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                         domain
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Eukaryota; Metazoa; C
ASHWORTH
                                                                            SEQUENCE FROM N.A. MEDLINE; 91376112.
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1-NOV-1996
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                                                                                             Sapiens (Human).
Iryota; Metazoa; Chordata; Craniata;
Iryota; Metazoa; Catarrhini; Hominid
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KRAFT A.;
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50444 MW;
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Catarrhini;
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Last sequence up
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Pred. No. 3.7e
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i; Hominidae;
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4e+02;
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Eukaryota; Metazoa;
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Eukaryota; Metazoa; Chordata; Craniata; Ver
Eukaryota; Primates; Catarrhini; Hominidae;
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Nucleic Acids Res. 18:7778-7178(1990).
EMBL; M73832; AAA35909.1; -.
EMBL; X54935; CAA38697.1; -.
Signal; Alternative splicing.
SIGNAL 1 22 POTENTIAL.
                                                                               MEDLINE; 98290545.
NAGASE T., ISHIKAWA
                                                                                                                                                                        SEQUENCE FROM N.A.
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"Cloning and characterization of BAI2 and
homologous to brain-specific angiogenesis
Cytogenet, Cell Genet, 79:103-108(1997).
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EMBL; AB005297; BAA23647.1; -
PFAM; PF00090; tsp_1; 5.
SEQUENCE 1584 AA; 173531 MW; 235A5C42 CRC32;
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EMBL; AB011122; BBAA25476.1; -.
PFAM; PF00090; tsp_1; 4.
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                                   J: Biol. Chem. 270:13133-1
EMBL; S78505; AAB34470.1;
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283 DSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAA 339

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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                  103 LANLNGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNWKDLTCRWTPGA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                223 ARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVE 282
                                                                                                        163 HGETFLHTNYSLKYKLRWYGODNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGS 222
207 VTSDHINFDPVYKVKPNPPHNLSVINSEELSSILKLTWTN-PSIKSVII-LKYNIQYRTK 264
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                                                                                                                                               91 FTDIASLNIQLTCNILTFGQLEQNVYGITIISGLPPEKPKNLSCIVNEGKKMRCEWDGGR 150
                                                                                                                                                                                                                       31 ISPESPVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVT 90
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                                                                       --ETHLETNFTLKSEWATHKFADCKAKRDT--PTSCTVDYSTVYFVNIEVWVEAENALGK 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                     103 LANINGSROOSGDNIVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGA 162
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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163 HGETFLHTNYSLKYKLRWYGODNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGS 222
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                                 91 FTDIASLNIQLTCNILTFGQLEQNVYGITIISGLPPEKPKNLSCIVNEGKKMRCEWDGGR 150
                                                                                                       31 ISPESPVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVT 90
                                                                                                                                         46 ISPODPTLLIGSSIQATCSIHG----DTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALA 102
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151 --ETHLETNFTLKSEWATHKFADCKAKRDT--PTSCTVDYSTVYFVNIEVWVEAENALGK 206

223 ARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVE

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 RLGAELQPGGRQQRLSDGTQESIITLPHLNHTQA--
                             TLNGRRLPSELSRLIN--TSTLALALANLNGSRQQSGDNLVCHARDGS---ILAGSCLYV 134
                                                              SLTWAALIILLL----PGSLEECGHISVSAPIVHLGDPITASCIIKQNCSHLDPEPQILW 63
                                                                                             SSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAE-GLYW 79
                                                                                                                                      l Similarity
97; Conser
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Pred. No. 1.5
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                    Local
                                                                                                                                     TYPE: AMINO ACID
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TORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 7 FILING DATE: 23-MAR-1990
                                                                                                                                                                                                                                                                     NAME: Hellwege, James REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPKDGQSHCCIPRKHLLLYQNMGIWVQAENALGISMSPQLCLDPMDVVKLEPPMLRIMDP 237
                                                                                                                                                                                                                                                                                                                                                       APPLICATION DATA:
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Arilington
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     Conservative
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                    11.3%;
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                    Score 254.5; DB 1
Pred. No. 1.3e-15;
     Mismatches
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                                    DB 1;
     148;
   Indels
                                  Length
                                    771;
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Gaps
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21 SSLWSPLLLCYLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAE-GLYW 79

15;

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NFORMATION FOR SEQ ID NO:
MOLECULE TYPE:
                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                      ELECOMMUNICATION INFORMATION:
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                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWS 334
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                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                           REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                APPLICATION DATA:
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                                                                                                                                                                                                              Hellwege,
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YSTEM: PC-DOS/MS-DOS
              protein
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Station
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Best Local :
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07-923-976-2
                TELEPHONE: 703-415-1500
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CURRENT APPLICATION DATA:
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                                                                                                           FILING DATE: 22-MAR-199:
TORNEY/AGENT INFORMATION
                                                      REFERENCE/DOCKET NUMBER:
                                                                      NAME: Hellwege, James REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                     OR APPLICATION DATA:
                                                                                                                                                                                                           APPLICATION NUMBER: JP 176629/1990
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                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 7
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                                                                                                                                                                                                                                                                                        APPLICATION DATA:
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703
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SYSTEM: PC-DOS/MS-DOS
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D. Box 2266 Eads Station
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                                                    514853
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Pred. No. 1.5e-15;
8; Mismatches 148;
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-923-976-2
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Patent No. 533267
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                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                  CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                  REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-082
                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 19911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 LCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIHGDTPGATAEG-LYWTLNGRRL- 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             DUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IP-KDLALFTPYEIWVEATNRLGSARSDYLTLDYLDYVTTDPP------PDVHVSRVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGDRQHHLPDGTQESLITLPHLNYT-QAFLFCLVPWEDSVQLLDQAELHAGYPPASPSNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                           RESSEE:
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                                                         Misrock, S. Leslie
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                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                     1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                               U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yancopoulos, George D. et al.
VENTION: Cell Free Ciliary Neurotrophic
VENTION: Factor/Receptor Complex
                                                                                                                                                                                                                                     PatentIn Release #1.0,
                                                                                                                                                                                                                                                                          IBM PC compatible
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INFORMATION:
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Pred. No. 2.3e-15;
6; Mismatches 16;
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Best Local Similarity 26.3
Matches 96; Conservative
                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: FRO COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/676,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 YMHLFSTIKYKVSISVSNALGH-NATAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTW 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 M-KDLTCRW-----TPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPK 202
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                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AAAAVVYAQRHSPQEAPHVQYERLGSDVTLPCGTANWDAAVT-----WRVNGTDLAPD-- 68
                                                                                                                                                                                                                                        COUNTRY:
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Misrock, S. Leslie
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The Ciliary Neurotrophic Factor Receptor
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Best Local Similarity
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                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stephen P.
US/08/449,329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6526-048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurotrophic Factor Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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; MOLECULE TYPE: US-08-449-329-2
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Best Local S
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                                                                                                                    320 GIYGSKKAGIWSEWS---
                                                                                                                                                                                                                                            168 YMHLFSTIKYKVSISVSNALGH-NATAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTW 226
                                                                                                                                                                                                                                                                                                                           121 YPKGFYCSWHLPTPTYIPNTFNVTVLHGSKIM ------VCEKDPAL-KNRCHI-R 167
338 GELGSG 343
                                   359 GEPSSG 364
                                                                              284 ----DNEIGTWSDWSVAAHATPWTEEPRHLTTEAQAAETTTSTTSSLAPPPTTKICDP-- 338
                                                                                                                                                            227 QTPSTWPDPESFPLKFFLRYRPLILDQWQHV-ELSDGTAHTITDAYAGKEYIIQVAAK--
                                                                                                                                                                                                  261 VSPPALKD-FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPF
                                                                                                                                                                                                                                                                                   203 DLALFT--PYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRW
                                                                                                                                                                                                                                                                                                                                                                   151 M-KDLTCRW-----TPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 RLLNTSTLALANLNGSRQQSGDNLVCHARDGSILAGS-CLYVGLPPEKPFNISCWSRN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 AHTAVI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US FILING DATE: 15-MAY-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 AAAAVVYAQRHSPQEAPHVQYERLGSDVTLPCGTANWDAAVT----WRVNGTDLAPD-- 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGISTRATION NUMBER: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMUNICATION INFORMATION: 212 790-9090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SPODPTLL----IGSSLOATCSIHGDTPGATAEGLYWTLNGRRLPSELS 91
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Pred. No. 6.8e-13;
                                                                                                                      -HPTAASTPRSERPGPGGGVCEPRG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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COUNTRY: U DRESSEE ESPONDENCE Application US/08445073 5849897 New York New York 1155 U.S.A. Squinto, Yancopoulos, Avenue Samuel Mark E The Ciliary Neurotrophic Factor Receptor Stephen P. of the Americas

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MOLECULE TYPE:
JS-08-445-073-2
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Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                   -US91-03896-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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                                                                        APPLICANT:
                                                                                                                          ERAL INFORMATION:
                                                                                                                                                                                                                                                                          359 GEPSSG 364
                                                                                                                                                                                                                                                                                                                 284 ----DNEIGTWSDWSVAAHATPWTEEPRHLTTEAQAAETTTSTTSSLAPPPTTKICDP-- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                261 VSPPALKD-FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 DLALFT--PYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRW 260
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               320 GIYGSKKAGIWSEWS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 YMHLFSTIKYKVSISVSNALGH-NATAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTW 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 M-KDLTCRW--
 ORRESPONDENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 RILINTSTLALALANINGSROOSGDNLVCHARDGSILAGS-CLYVGLPPEKPFNISCWSRN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AAAAVVYAQRHSPQEAPHVQYERLGSDVTLPCGTANWDAAVT-----WRVNGTDLAPD-- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 AHTAVI-----SPODPTLL----IGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/676,647 FILING DATE: 28-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                         LICANT:
               LICANT: Yancopoulos, George D.

JE OF INVENTION: The Ciliary Neurotrophic Factor Receptor

JER OF SEQUENCES: 15
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                                                                                                                                                                                                                                                                                                                                                                                            QTPSTWPDPESFPLKFFLRYRPLILDQWQHV-ELSDGTAHTITDAYAGKEYIIQVAAK--
                                                                                                                                                                                                                                              GELGSG 343
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                                                                                                                                               Application PC/TUS9103896
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                                                                                                              Davis, Samuel
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                                                                       Squinto, Stephen P. Furth, Mark E.
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26.2%;
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Pred. No. 6.8e-13;
2; Mismatches 149
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Best Local S
                  08-685-118-2
equence 2,
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                                                                                        338
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                                                                                                                          359 GEPSSG 364
                                                                                                                                                        284 ----DNEIGTWSDWSVAAHATPWTEEPRHLTTEAQAAETTTSTTSSLAPPPTTKICDP-- 338
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                                                                                                                                                                                                                                                                                                     168 YMHLFSTIKYKVSISVSNALGH-NATAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTW
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                                                                                                                                                                                                                                                                                                                                       203 DLALFT--PYEIWYEATNRLGSARSDYLTLDYLDYYTTDPPPDVHVSRYGGLEDQLSVRW 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 RILINTSTLALALANINGSRQQSGDNLVCHARDGSILAGS-CLYVGLPPEKPFNISCWSRN 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 AHTAVI----SPQDPTLL----IGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELS 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFERENCE/DOCKET NUMBER:
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                                                                                        GELGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      *LLNGSQLV-----LHGLELGHSGLYACFHRDSWHLRHQVLLHVGLPPREPV-LSCRSNT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
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AMINO ACID
Application US/08685118
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 220.5; DB Pred. No. 6.8e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                             -HPTAASTPRSERPGPGGGVCEPRG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                -VCEKDPAL-KNRCHI-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 372;
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                                                                                                                                                                                                                                                                                                       226
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19;

167

tent No.

ITLE OF INVENTION:

Gubler, Ulrich A Presky, David H JENTION: RECEPTORS FOR HUMAN IL-12

19;

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MOLECULE TYPE: protein -08-685-118-2
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Best Local Similarity
                                                                                                                                   08-915-495-2
                                                                                                                    equence 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                           300 FX---
                                                                                                                                                                                                                 321 IYGSKKAGIWSEWSHPTAASTPRSERPG 348
                                                                                                                                                                                                                                                                                                               198
                                                                                                                                                                                                                                                                                                                                                                  141 VACTWERGR--DTHLYTEYTLQLSGPKNLTWQKQCKDIYC-DYLDFGINLTPESPESNFT 197
                                                                                                                                                                                                                                                                                                                                                                                                154 LTCRWTPGAHGETFLHTNYSLKY----KLRWYGQ--DNTCEEYHTVG------PHSCHI 200
                                                                                                                                                                                                                                                                            261 VSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFG 320
                                                                                                                                                                                                                                                                                                                                      201 PKDLALFTPYEIWVEATNRLGSARSDYLTLDYLDYYTTDPPPDVHYSRYGGLEDQLSYRW 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 NTSTLALALANLNGSRQQSGDNLYCHARDGSILAGSCLYYGLPPEKPFNISCWSRNMK-D 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 LLIGSSLQATCSIHGDTPGATAEGLYWTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                95 GTTLFVCKLACINSDEIQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 ILLGSTVNITCSL-----KPRQGCFHYSRRNKLILYKFDRRINFHHGHSLNSQVTGLPL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Polo---
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                                                                                                   No.
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                                                                                     INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
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                                                                                                                    Application US/08915495
                                                                                                                                                                                          KGSWSDWSESLRAQTPEEEPTG 323
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                                                          Gubler, Ulrich A
Presky, David H
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Hoffmann-La Roche Inc.
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                                                                                                                                                                                                                                                                                                           VTAVNSLGSSSSLPSTFTFLDIVRPLPPWDIRIKFQKASVSRCTLYW 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.7%;
                                            RECEPTORS
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Pred. No. 4.
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                                          FOR HUMAN
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Best Local
                                                                   APPLICANT:
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                                                                                  INFORMATION:
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                                                                                                            Application US/08419652
                                                  Gubler, Ulrich
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INFORMATION FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                              141 VACTWERGR--DTHLYTEYTLQLSGPKNLTWQKQCKDIYC-DYLDFGINLTPESPESNFT
300 LY----KGSWSDWSESLRAQTPEEEPTG
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                                                                                                                                                                                                                                                                                                                                                                                                                          53 LLIGSSLQATCSIHGDTPGATAEGLYWTL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/915,495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILING DATE
                                                                                                                                                                                                                                                                                                                                              NTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMK-D 153
                                     IYGSKKAGIWSEWSHPTAASTPRSERPG
                                                                                                               VSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFG 320
                                                                                                                                                                                         PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRW 260
                                                                                                                                                                                                                                                                    LTCRWTPGAHGETFLHTNYSLKY----KLRWYGQ--DNTCEEYHTVG-----PHSCHI 200
                                                                                                                                                                                                                                                                                                            GTTLFVCKLACINSDEIQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                         RDEGLYLLNRLRYRPSNSRLWNMVNVTKAKGRHDLLDLKPFTEYEFQI-SSKLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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Gaps

14;

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fmann-La Roche Inc

Anne

INTERLEUKIN-12 RECEPTOR

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Query Match
Best Local Similarity 31.00
"""thes 68; Conservative
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243 DYHYSRYGGLEDQLSYRWYSPPALKDFLFQAKYQIRYRYE-DSYDWKYYDDYSNQT-SCR 300
                                                                                                                                                                                                                                                                            137 PPEKPFNISC-WSRNMKDLTCRWTPGAHGETFLHTNYSLK-YKLRWYGQ---DNTCEEYH 191
                                                                            121 EAAPPQAGCLQ----LCW--EPWQPGLHINQKCELRHKPQRGEASWALVGPLPLEALQYE 174
                                                                                                                                                                                            192 TVGPHSCHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVV------TTDPPP 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
URRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC compatible
                                                                                                                                                         61 KDGQSHCCIPRKHLLLYQNMGIWVQAENALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                       3 PPAIPHNLSCLMNLTTSSLICQWEPGP--ETHLPTSETLKSFKSRGNCQTQGDSILDCVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: CD 9174
LECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 340 Kingsland Street CITY: Nutley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICATION NUMBER:
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DATE: 31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER: US 08/094,713
19-JUL-1993
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                                                                                                                                                                                                                                                                                                                        9.6%; Score 216.5; DB 2; 31.8%; Pred. No. 3.3e-12; tive 31; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Represents residues 98 to
731 of human granulocyte colony-stimulating
factor-receptor."
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                                                                                                                                                                                                                                                                                                                    Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                             Length 602;
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Search completed: September 16, 1999, 20:41:06 Job time: 5435 sec

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:05; Search time 49.27 Seconds (without alignments) 335.844 Million cell updates/sec

Perfect score: Sequence:

US-09-037-657-13
2251
1 MPAGRPGPVAQSARRPPRPL.....WRAWMQKSHKTRNQVLPAKL 413

Scoring table: BLOSUM62

Database : Searched: 122810 seqs, 40065486 residues

PIR_60:*
1: pir1:*
2: pir2:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

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PC4184 JC4897 S37622 JX0312 JC2181 S74225
leptin receptor, O leptin receptor, O leptin receptor, O proto-oncogene - m differentiation-st differentiation-st leptin receptor, i

ALIGNMENTS

CLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLP: YHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVL:	SULT 1 Olact receptor long form precursor, hepatoma and breast cancer cell colactin receptor long form precursor, hepatoma and breast cancer cell species; Homo sapiens (man) Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-Accession: A40144 BOUTIN, J.M.; Edery, M.; Shirota, M.; Jolicoeur, C.; Lesueur, L.; Ali 1. Endocrinol. 3, 1455-1461, 1989 Title: Identification of a cDNA encoding a long form of prolactin rec accession: A40144 MOJECULE type: mrNA molecule type: mrNA mesidues: 1622 -8000
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J. Biol. Chem. 270, 13133-13137, 1995
A;Title: Prolactin receptor antagonists that inhibit the A;Reference number: A57018; MUID:95286597
A;Accession: A57018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prolactin receptor - human (fragment)
C;Species: Homo sapiens (man)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
C;Accession: A57018
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A;Map position: 5q11-5q11
C;Keywords: glycoprotein; membrane protein
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Matches
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                                       178 YLVQVRCKP-----DHGYWSAWSPATFIQIP 203
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                                                                                                                                                                                                                                                                                             Match 14.4%; Score 324.5; DB 2

LOCAL SIMILATITY 38.0%; Pred. No. 2.8e-19;

les 81; Conservative 25; Mismatches 90
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                                                             YFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                RKPYLWIKWSPPTLIDLKTGWETLLYEIRLKPEKAAEWE-IHFAGQQTEFKILSLHPGQK 177
                                                                                                                                                             NSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLELAV-EVKQPED 118
                                                                                                                                                                                HSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPDDVHVSRVGGLED 254
                                                                                                                                                                                                                                             LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTSDHINFDPVYKVKPNPPHNLSVINSEELSSILKLTWTN-PSIKSVII-LKYNIQYRTK
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                                                                                                                              QLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV 309
                                                                                                                                                                                                                           LPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLMHECPDYITGGP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIRC----MKEDGKGYWSDWSEEASG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --ETHLETNETLKSEWATHKFADCKAKRDT--PTSCTVDYSTVYFVNIEVWVEAENALGK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTDIASLNIQLTCNILTFGQLEQNVYGITIISGLPPEKPKNLSCIVNEGKKMRCEWDGGR
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                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                           Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth of breast cancer cell
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C;Accession: A44257
R;Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A;Title: Molecular cloning and characterization of the rat liver IL-5 signal transduc A;Reference number: A44257; MUID:93052397
A;Accession: A44257
A;Status: prellminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-918 <WAN>
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("Species: Mus musculus (bouse mouse)

("Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change (
CAccession: 149699; 148370

R;Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.

J. Immunol. 148, 4066-4071, 1992

A;Title: Molecular cloning of a murine II-6 receptor-associated A;Reference number: 148370; MUID:92291532

A;Accession: 149699
A; Note: sequence extracted from NCBI backbone (NCBIP:118488) C; Keywords: transmembrane protein
                                  A; Experimental source: liver A; Note: sequence extracted f:
                                                                                                                                                                                                                                                                                                           interleukin-6 signal transducing molecule gpl30 - rat
c;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #t
C;Accession: A44257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: gp130
C;Keywords: gl
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A; Residues: 1-917 < RE2>
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A; Residues: 1-917 < RES>
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Best Local Similarity 29.69
92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --ETYLETNYTLKSE--WATEKFPDCQSKHGT---SCMVSYMPTYYVNIEVWVEAENALG
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                                                                                                                                                                                                                                                                                                                                18-Nov-1994 #text_change 16-Feb-1997
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:05; Search time 49.27 Seconds (without alignments)
335.844 Million cell updates/sec

Title: US-09-037-657-13
Perfect score: 2251
Sequence: 1 MPAGRPGPVAQSARRPPRPL......WRAWMQKSHKTRNQVLPAKL 413

Searched: 122810 segs, 40065486 residues

Scoring table:

BLOSUM62

Database : PIR_60:* 1: pir1:* 2: pir2:* 3: pir3:*

pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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,	recepto	C4797		894	8.4		95
	lactogen receptor	34031		Too	0.4) <u>-</u>	, ,
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	D	34898		837	11.2	52.	21
	granulocyte colony	38252		863		54.	20
	granulocyte colony	38252		771	11.3	54.	19
	granulocyte colony	H0329		783		54.	18
	'n	51086		630	11.6	61.	17
	C,	45971		581		302.5	16
	5	Q1655		831	13.6	30	15
	5	153269		809	13.7	97.	14
	i,	77525		292	13.7	07.	13
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	Description	ID	DB 1	engt	7	H	NO.
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ALIGNMENTS

in receptor long form precursor, hepatoma and breast cancer cells - human

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F;25-622/Product: prolactin receptor, long form #status predicted <MAT>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane glycoprotein gp130 precursor - human
                                                                                                                                                                                      Reference number: Accession: A36337
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Best Local Similarity
                                                                                              Molecule type: mRNA
Residues: 1-918 <HIB>
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                                                         Cross-references: GB:M57230; NID:g186353; PID:g186354
                                                                                                                                                        Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Map position:
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Residues: 1-622 <BOUD
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                                                                                                                                                                                                                        le: Molecular cloning and expression of an IL-6 signal transducer, gp130.
erence number: A36337; MUID:91084844
                                                                                                                                                                                                                                                                                            i, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
53, 1149-1157, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 LAV-EVKOPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGOOTE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 FKILSLHPGQKYLVQVRCKP------DHGYWSAWSPATFIQIP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 CRLAGIKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 LELNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLM 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 HECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLE 132
GDB:IL6ST; GP130
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                                                                                                                                                                                                                                                                                                                                                                                #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998
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A;Map position: 5q11-5q11
C;Keywords: glycoprotein; membrane protein
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A;Title: Prolactin receptor antagonists that inhibit
A;Reference number: A57018; MUID:95286597
A;Accession: A57018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Homo sapiens (man)
Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession:
                                                                                                                                                                                                                                                                                       Matches
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Residues: 1-206 <RES>
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Best Local (
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     178
                                   310 YFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                        119
                                                                                                          255
                                                                                                                                                                       196 HSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLED
                                                                                                                                                                                                                                              136 LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGODNTCEEYHTVGP 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 ISPQDPTLLIGSSLQATCSIHG----DTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALA 102
                                                                                                                                                                                                              N
                                                                                                      QLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV
                                                                                                                                         NSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLELAV-EVKQPED
                                                                                                                                                                                                              LPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLMHECPDYITGGP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STPRSERP 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIRC----MKEDGKGYWSDWSEEASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTSDHINFDPVYKVKPNPPHNLSVINSEELSSILKLTWTN-PSIKSVII-LKYNIQYRTK
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YLVQVRCKP-----DHGYWSAWSPATFIQIP 203
                                                                    RKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTEFKILSLHPGQK 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WELLS,
                                                                                                                                                                                                                                                                                       81;
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Pred. No. 8.6e-19;
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R; Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M. Genomics 14, 666-672, 1992
A; Title: Molecular cloning and characterization of the A; Reference number: A44257; MUID:93052397.
A; Accession: A44257
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                         A; Experimental source: live A; Note: sequence extracted
                                                                         A; Molecule type: mRNA
A; Residues: 1-918 <WAN>
                                                                                                                                                                                                                                                                       C; Accession:
                                                                                                                                                                                                                                                                                            interleukin-6 signal transducing molecule gp130 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #t
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                                                                                                                  A; Status: preliminary; not compared with conceptual translation
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A; Reference number: I48370; MUID:92291532
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;Note: sequence extracted from NCBI backbone (NCBIP:118488)
| Reywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Mus musculus (house mouse)
Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 07-Feb-1997
Accession: I49699; I48370
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Best Local (
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Residues: 1-917 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: translated from GB/EMBL/DDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 HGETFLHTNYSLKYKLRWYGOD-NTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 AST--PRSERP 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 EDSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 LANLNGSROOSGDNLYCHARDGSILAGSCLYYGLPPEKPFNISCWSRNMKDLTCRWTPGA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 GTTYEDRPSRP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 · KVSSESINFDPVDKVKPTPPYNLSVTNSEELSSILKLSWVSSGL--GGLLDLKSDIQYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 SARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 FTDVVLPSVQLTCNILSFGQIEQNVYGVTMLSGFPPDKPTNLTCIVNEGKNMLCQWDPGR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 ISPQDPTLLIGSSLQATCSIHG---DTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 IYPEFPVVQRGSNFTAICVLKEACLQHYYVNASYIVWKTNHAAVPREQVTVINRTTSSVT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ETYLETNYTLKSE--WATEKFPDCQSKHGT---SCMVSYMPTYYVNIEVWVEAENALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDASTWIQVPLEDTMSPRTSFTVQDLKPFTEYVFRIR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148, 4066-4071,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .-917 <RE2>
                                                                                                                                                                                                                                                                                         1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                  liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.2%; Score 319.5; DB 2; 29.6%; Pred. No. 5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NID: g840816; PID: g840817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor-associated signal transducer, g
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                                                                                                                                                                                              of the rat liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIKDSGK-GYWSDWSEEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                              IL-6
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                                                                                                                                                                                           signal
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RESULT

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actogen receptor 1 - rat
;Species: Rattus norvegicus (Norway rat)
;Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 10-Sep-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Residues: 1-830 <CHE>
;Cross-references: EMBL:U07694; NID:g466381; PID:g466382
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title: Cloning, expression, and mutational analysis of the Reference number: I50455; MUID:94283267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen, X.; Horseman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          olactin receptor - pigeon
Species: Columba livia (domestic pigeon)
Date: 13-Sep_1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rinology 135, 269-276, 1994
                                                                                                                                                               406
                                                                                                                                                                                               310
                                                                                                                                                                                                                                348
                                                                                                                                                                                                                                                                                                         196 HSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDDPPDV--HVSRVGGL 252
                                                                                                                                                                                                                                                253 EDQLSVRWYSFFALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKFGTV 309
                                                                                                                                                                                                                                                                                                   288
                                                                                                                                                                                                                                                                                                                                                                      231
                                                                                                                                                                                                                                                                                                                                                                                      137 PPEKPENISCWSRNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                      YFVQVRCNPFGIYGSKKAGIWSEWS 334
                                                                                                                                                                                                                                                                                   NSCYFDKKHTSFWTIYNITYKATNEIGSNVSDPLYVDVTYIVQTDPPVNVTLELKKTVNR 347
                                                                                                                                                                                                                 KPYLVLTW-SPPPLADVRSGWLTLDYELRLKPEEAEEWETI-FVGQQTHYKWFSLNPGKK 405
                                                                                                                                                                                                                                                                                                                                                    PPEKPTIIKCRSPEKETFTCWWKPGSDGG---HPTNYTLLYSKEGEERVYECPDYKTAGP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDASTWIQVPLEDTVSPRTSFTVQDLKPFTEYVFRIR----SIKENGK-GYWSDWSE-EA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVSSEPINFDPVDKVKPSPPHNLSVTNSEELSSILKLAWVNSGL--DSILRLKSDIQYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SARSDYLTLDYLDYYTTDPPPDVHYSRYGGLEDQLSYRWYSPPALKDFLFQAKYQIRYRY 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- ETYLETNYTLKSE--WATEKFPDCRTKH--GTSSCMMGYTPIYFVNIEVWVEAENALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGETFLHTNYSLKYKLRWYGQD-NTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASTPRSERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTDVVFQNVQLTCNILSFGQIEQNVYGITILSGYPPDIPTNLSCIVNEGKNMLCQLDPGR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISPODPTLLIGSSLOATCSIHG---DTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IYPEFPVVQRGSNFTATCVLKEKCLQVYSVNATYIVWKTNHVAVPKEQVTVINRTASSVT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                       76;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
   E.; Tsai-Morris,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347
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                                                                                                                                                          -DHHGSWSEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 314; DB 2;
Pred. No. 1.2e-17;
29; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 7.3e-18; 1; Mismatches 145;
                                                                                                                                                          424
   C.H.;
   Hu,
 Z.Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                             82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 830,
Dufau, M.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prolactin receptor.
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A;Residues: 1-610 <SHI>
A;Cross-references: GB:M57668; NID:g206366; PID:g206367; GB:M60728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Shirota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, Mol. Endocrinol. 4, 1136-1143, 1990
A;Title: Expression of two forms of prolactin receptor in rat ovary and liver.
A;Reference number: A36116; MUID:91155946
A;Accession: A36116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prolactin receptor 2 precursor - rat
c;Species: Rattus norvegicus (Norvay rat)
C;Date: 28-Mar_1991 *sequence_revision 28-Mar-1991 *text_change 10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          皮
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 168, 415-422, A/Title: Isolation and characterization of to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-610 < ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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A;Accession: A34631
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local (
                                                                 184 TOFKVFDLYPGQKYLVQTRCKP-----DHGYWSRWSQESSVEMP
                                                                                                    297 TSCRLAGIKPGTYYFYQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                            126 RNLTL-EVKOLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ
                                                                                                                                                                                                                                                              185 NT--CEEXHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP 241
                                                                                                                                                                                                                                                                                                                                 125 SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGOD 184
                                                                                                                                                                                242 PDVHVSRVGGLEDQLSVRWY--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 296
                                                                                                                                                                                                                                                                                                          15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                                                                                                                                                                                                        66 TIYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 RNLTL-EVKOLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGOD 184
                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 TIYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOFKVFDLYPGQKYLVQTRCKP-----DHGYWSRWSQESSVEMP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80;
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.9%; Score 312; DB 2; 35.4%; Pred. No. 1.2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUID: 90241201
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                                                                                                                                                                                                                                                                                                                                                                                            Score 312; DB 2; Pred. No. 1.2e-17; 5; Mismatches 85;
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prolactin receptor Nb2 precursor -

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                                                                                                                                                                                                                                                                                  A; Title: Cloning and expression of the rat A; Reference number: A29884; MUID:88165059 A; Accession: A29884
                                                                                                                                                                                                                                                                                                                                                                                                                    prolactin receptor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
                                                                                                                                                                                                               Cross-references: GB:M19304; NID:g206364; PID:g206365; Reywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                  Boutin,
                                                                                                                                                                                                                                                                                                                                                                                   Species: Rattus norvegicus (Norway rapate: 30-Sep-1989 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:U07567; NID:g641963; PID:g641964
Experimental source: Nb2-11C cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 400, 40110 average immune cell. Title: A prolactin-dependent immune cell. Paference number: A41070; MUID:92041834
                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                   Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                    Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title: Differential signal transduction
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                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: mRNA
                                                                                                                                                                                                                                                     Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: A41070
                                                                                                                                                                                  .9/Domain: signal sequence #status predicted <SIG>
310/Product: prolactin receptor #status predicted
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   185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 RNLTL-EVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLLKGOS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translated from GB/EMBL/DDBJ
NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP
                                    SLLKGQS---
                                                              SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOFKVFDLYPGOKYLVOTRCKP------DHGYWSRWSQESSVEMP 222
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                                                                                                                                                                                                                                                1-310 <BOU>
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                                                                                                                                                                                                                                                                                                                                                                       A29884
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269, 26076-26082, 1994
                                                                                                                                                                                                                                                                                                                                                    Jolicoeur,
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                                                                                                Conservative
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89 #sequence_revision 30-Sep-1989 #text_change 20-Mar-1998
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92 #sequence_revision 12-Jun-1992 #text_change 10-Sep-1997
                               -PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                                                                                                13.98;
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                                                                                                                Score 312; DB 2
Pred. No. 5e-18;
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5; Mismatches
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Pred. No. 7
                                                                                                Mismatches .
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                                                                                                                                                                                                                                                                                                                                               J.; Edery, M.;
                                                                                                                              Length 310;
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                                                                                                Indels
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                                                                                             Gaps
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                             Mol. Endocrinol.
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             A; Title: Expression
                                              ;Davis, J.A.;
                                                              Accession:
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F;25-616/Product: prolactin receptor 2
F;235-258/Domain: transmembrane #status
F;59,104,132,347,389,411/Binding site:
prolactin receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 41-58,'X',60-66;90-93,'X',95-96,'X',98-103,'X',105,'NX',108;150-154,'XX'
A; Note: the amino end of the mature protein was blocked
C; Keywords: blocked amino end; glycoprotein; transmembrane protein
                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Int. J. Blochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Edery, M.; Jolicoeur, C.; Levi-Meyrueis, C.; Dusanter-Fourt, Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prolactin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,..... furification and partial sequence of the rabbit mammary gland Reference number: A60380; MUID:91146782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Title: Identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Waters,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Oryctolagus cuniculus (domestic rabbit)
Date: 07-Sep-1990 *sequence_revision 07-Sep-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPH 196
                                                                                                                                                                                                          311 FVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                          144 KPYLWYKWLPPTLYDYRSGWLTLQYEIRLKPEKAAEWE-THFAGQQTQFKILSLYPGQKY
                                                                                                                                                                                                                                                                                                                                                                                                   197
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                                                                                                                                                                   203 LVQVRCKP---
                                                                                                                                                                                                                                                                                                   256 LSYRWYS--PPALKDF---LFQAKYQIRYRYEDSYDWKYYDDYSNQTSCRLAGLKPGTYY 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ
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                                                                                                12
                                                                                                                                                                                                                                                                                                                                                                                               SCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQ
                                                                                                                                                                                                                                                                                                                                                   SCYFSKKHTSIWTIYIITVNATNQMGSSVSDPRYVDVTYIVEPDPPVNLTL-EVKHPEDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor 2 precursor - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                               PPGKPFIFKCRSPEKETFTCWWRPGADGG--LPTNYTLTYHKEGETITHECPDYKTGGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNLTL-EVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A30304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .; Spencer, S.A.;
em. 22, 1089-1095,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                 --- DHGFWSVWSPESSIQIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
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j site: carbohydrate (As
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 307.5; DB 2;
Pred. No. 2.8e-17;
"""" tches 90;
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2 #status predicted <MAT>
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Bout

Linzer, D.I.H. 1. 3, 674-680,

of multiple forms of 157699; MUID:89261824

the

prolactin

receptor

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mouse

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02-Aug-1996

#text_change

02-Aug-1996

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R;Davis, J.A.; Linzer, D.I.H.
Mol. Endocrinol. 3, 674-680, 1989
A;Title: Expression of multiple forms of the prolactin receptor A;Reference number: 157699; MUID:89261824
A;Accession: 177525
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A;Status: preliminary; translated from A;Molecule type; mRNA
A;Residues: 1-303 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Mus musculus (house mouse)
Date: 02-Aug-1996 #sequence_revision
Accession: 177525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB: M22958; NID: g200479; PID: g200480
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Molecule type: mRNA ; Residues: 1-292 < RES>
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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                                                                                                                                                                                                               NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGODNT--CEEYHTVGPHSCHIPKD-LAL 206
                                                                                                                                                                                                                                                                                            LSRLLNTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSR 149
----DHGYWSRWGQEKSIEIP 222
                               YGSKKAGIWSEWSHPTAASTP 342
                                                           TITDVKTGWFTMEYEIRLKSEEADEWE-IHFTGHQTQFKVFDLYPGQKYLVQTRCKP---
                                                                                         ALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 321
                                                                                                                           WKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP
                                                                                                                                                                                          DKETFTCWWNPGSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI 90
                                                                                                                                                                                                                                                                    MSSALAYMLLVLSISLLNG---QS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKETFTCWWNPGSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTPYEIWVEATNRLGSARSDVLTLDYLDVVTTDPPPDVHVSRVGGLEDQLSVRWVS--PP 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNT--CEEYHTVGPHSCHIPKD-LAL
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85; Conserv
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                                                                                                                                                                                                                                                                                                                                 13.7%; Score 307.5; DB 2; 32.6%; Pred. No. 1.1e-17; tive 37; Mismatches 92;
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Pred. No. 1.1e-17;
7; Mismatches 92;
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R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prola
A;Reference number: JQ1655; MUID:93075121
                                                                                               prolactin receptor precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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A; Residues: 1-557, 'F', 559-608 <EDE>
A; Cross-references: EMBL: X73372; NID: g312696; PID: g312697
C; Comment: Prolactin receptor have long form and short form which are resulted from C; Comment: This long form receptor is capable of transducing a signal to milk protein c; Keywords: receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
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A:Title: Cloning and sequencing of the cDNA encoding the murine mammary A;Reference number: JT0671; MUID:94085788
A;Accession: JT0671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Edery, M.; Pezet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Changes in prolactin receptor expression A; Reference number: I53269; MUID: 93307149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endocrinology 133, 224-232,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor. Reference number: S34356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Residues: 1-608 <MOO>
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;Residues: 1-608 <RE
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nes 85; Conserv
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                                                                                                                                                                                                                                                                                              YGSKKAGIWSEWSHPTAASTP 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTPYEIWVEATURLGSARSDYLTLDYLDYVTTDPPPDVHVSRVGGLEDQLSVRWVS--PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKETFTCWWNPGSDGG--LPINYSLTYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI 90
                                                                                                                                                                                                                                                       ----DHGYWSRWGQEKSIEIP
                                                                                                                                                                                                                                                                                                                                   TITDVKTGWFTMEYEIRLKSEEADEWE-IHFTGHQTQFKVFDLYPGQKYLVQTRCKP---
                                                                                                                                                                                                                                                                                                                                                                        ALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 321
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                     prolactin
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Residues: 1-831 <TAN>
Cross-references: DDBJ:D13154; NID:g222848; PID:d1002939; PID:g222849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ywords: glycoprotein; transmembrane protein
23/Domain: signal sequence #status predicted <SIG>
1-831/Product: prolactin receptor #status predicted <MAT>
19-462/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                       310 YFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSER 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 PPEKPTIIKCRSPEKETETCWWKPGLDGG---HPTNYTLLYSKEGEEQVYECPDYRTAGP 286
405 YIIQIHCKP-----DHHGSWSEWSSENYIQIPNDFR 435
                                                                                                                                                                                                                                                                                                                               347 KPYLVLTW-SPPPLADVRSGWLTLEYELRLKPEEGEEWETI-FVGQQTQYKWFSLNPGKK 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 EDQLSVRWVSPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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Search completed: September 16, 1999, 20:42:06
Job time: 5399 sec

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd
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OM protein protein search, using sw model

Run on: September 17, 1999, 03:10:11; 1 ; Search time 35.09 Seconds (without alignments)
332.710 Million cell updates/

Million cell updates/sec

Perfect score: Sequence: Title: US-09-037-657-13 2251

1 MPAGRPGPVAQSARRPPRPL.....WRAWMQKSHKTRNQVLPAKL 413

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database : SwissProt_37:*

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution. being printed

SUMMARIES

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Query Match Best Local S Matches 84

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Conservative

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Score 331; DB 1; Pred. No. 1.2e-19; 7; Mismatches 95;

Length 622; Indels

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  he European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALI S., GOULD D., DJIANE J., KELLY P.A.; Identification of a cDNA encoding a long foin human hepatoma and breast cancer cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 90114212.
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01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PROLACTIN RECEPTOR PRECURSOR (PRL-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOUTIN J.-M., EDERY M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IOMO SAPIENS (HUMAN).
SUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235
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SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
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E; PS00340; RECEPTOR_CYTOKINES_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                             email to license@isb-sib.ch
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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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                                                                                                                                                                                            IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT (BY SIMILARITY).

-1- SUBGUIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

-1- SUBGUIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

-1- SUBGUIT: HOLOTIY: FOUND IN ALL THE TISSUES AND CELL LINES EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.

-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS.

-1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.

-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

-1- SIMILARITY: DOMAINS.

-1- SIMILARITY: DOMAINS.
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15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (
6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 1
RECEPTOR) (CDW130) (CD130 ANTIGEN).
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                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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BRAVO J., STAUNTO
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
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HIBI M., MURAKAMI M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995
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                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                        G186354;
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n IL-6 signal
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region of gpl30.";
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130) (GP130)
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Best Local S
Matches 88
Q00560;
Q00560;
Q00560;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
                                                                                         MOUSE
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                                                                                                                                                                                                                                      --ETHLETNETLKSEWATHKFADCKAKRDT--PTSCTVDYSTVYFVNIEVWVEAENALGK
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Pred. No. 3e-19;
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7CC06F05 CRC32;
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SAITO M., YOSHIDA K., HIBI M., TAGA T., KISHIMOTO T.;

"Molecular cloning of a murine IL-6 receptor-associated signal amplecular cloning of a murine in the description of the signal amples of the sign
                                                                                                                                                                                                         CARBOHYD
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EMBL; M83336; G193592; -.
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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transducer, gp130, and its regulated expression I. IMMUNOL. 148:4066-4071(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,
SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED
EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE IG-LIKE DOMAIN.
SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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    102452 MW;
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FIBRONECTIN TYPE-III.
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Query Match

14.28;

Score 319.5;

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Length 917;

EMBL; M92340;

NOT_ANNOTATED_CDS

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                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     - I - SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IL6B_RAT
P40190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transducing molecule, gp130.";
GENOMICS 14:666-672(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE: 93052397.
WANG I., NESBITT J.E., FUENTES N.L., FULLER G.1
"Molecular cloning and characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA,
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATTUS NORVEGICUS (RAT).
EUKARYOTA: METAZOA; CHOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
1NTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 EDSYDWKYV---DDYSNQTSCRLAGLKPGTYYFYQYRCNPFGIYGSKKAGIWSEWSHPTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 SARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 HGETFLHTNYSLKYKLRWYGOD-NTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 LANLNGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNNKDLTCRWTPGA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 FIDVVLPSVQLICNILSFGQIEQNVYGVIMLSGFPPDKPINLICIVNEGKNMLCQWDPGR
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                                                                                                                                                                                                                                                                                                    FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL DOES NOT BIND IL-6. MAY HAVE A ROLE IN SUBGRIVENIC DEVELOPMENT (BY SIMILARITY).

SUBGRIVANIC DEVELOPMENT (BY SIMILARITY).

SUBGRIVI: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
                                                                                                                                                                                                 SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                       ONE IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                              AND ENDOTHELIAL CELLS
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e rat liver IL-6 signal
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92; Conservative
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                                 97 (REL. 35, CREATED)
97 (REL. 35, LAST SEQ
98 (REL. 36, LAST ANN
RECEPTOR PRECURSOR (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 317.5; | Pred. No. 2.6e | State | Pred. No. 2.6e | 
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                                            ON UPDATE)
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             406 YIVQIHCKP--
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use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; COLUMBIFORMES; COLUMBIDAE; COLUMBA.
                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00041
HSSP; P16471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HORSEMAN N.D.;
                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression,
                                                                                         36
75
100
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132
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316
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RECEPTOR_CYTOKINES_2;
                                                    94507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mutational analysis of the pigeon prolactin
                                                                                                                                                                                                                                                                                                                                                                                                          GLYCOPROTEIN;
                                                    ME.
                                                  POTENTIAL. ; SEFADD51
                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                   POTENTIAL.
                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                          FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                         FIBRONECTIN
                                                                                                                                                                                                                                                                                                                                                   PROLACTIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                            POTENTIA
                                                                                                                                                                                                                                                        IBRONECTIN TYPE-III
                                                                                                                                                                                                                       SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL; REPEAT
                                                  CRC32
                                                                                                                                                                                                                                                                                      C (POTENTIAL).
N TYPE-III.
N TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions
 830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              commercia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              way
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310 YFVQVRCNPFGIYGSKKAGIWSEWS 334
                                                                                                                                                                                               HSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDV--HVSRVGGL
                                                                               KPYLVLTW
                                                                                                                  EDQLSVRWVSPPALKDF --- LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV
                                                                                                                                                                                                                                         PPEKPTIIKCRSPEKETFTCWWKPGSDGG---HPTNYTLLYSKEGEERVYECPDYKTAGP
                                                                                                                                                                                                                                                                            PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP 195
                                                                                                                                                         NSCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLYVDVTYIVQTDPPVNVTLELKKTVNR
                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                               SPPPLADVRSGWLTLDYELRLKPEEAEEWETI-FVGQQTHYKMFSLNPGKK
-- DHHGSWSEWS
                                                                                                                                                                                                                                                                                                                                      13.9%;
                                                                                                                                                                                                                                                                                                                   Score 314; DB 1;
Pred. No. 4.4e-18;
9; Mismatches 82;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                            405
                                                                                                                  309
                                                                                                                                                         347
                                                                                                                                                                                                 252
                                                                                                                                                                                                                                         287
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                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                            Differential signal transduction of the short, Nb2, and long prolactin receptors. Activation of interferon regulatory factor-1 and ell proliferation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHIROTA M., BANVILLE D., ALI S., JOLICOEUR C., BOUTIN J.M., EDERY M., DJIANE J., KELLY P.A.; "Expression of two forms of prolactin receptor in rat ovary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDLINE; 92041834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OUTIN J.-M., JOLICOEUR C., OKAMURA H., GAGNON J., EDERY M., BIROTA M., BANVILLE D., DUSANTER-FOURT I., DJIANE J., KELLY P.A.; Cloning and expression of the rat prolactin receptor, a member of the growth hormone/prolactin receptor gene family."; ELL 53:69-77(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A. (FORM NB2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IOCHEM. BIOPHYS. RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEAL K.D., YU-LEE L.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A. (FORM NB2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OUENCE OF 281-610 FROM N.A.
NIVILLE D., STOCCO R., MURTHY K.K., BOIE
JEMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                         BIOL. CHEM. 269:
- EUNCTION: THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLINE; 88165059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   solation and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDLINE; 91155946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        )5710; Q63451; Q63723; Q62832; Q64274; Q63-
L-NOV-1988 (REL. 09, CREATED)
L-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
L-NOV-1997 (REL. 35, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLR_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAIN-SPRAGUE-DAWLEY; TISSUE-OVARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prolactin-dependent
prolactin receptor."
                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PROFESPLICING OF THE PRLR GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOL. CHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DUENCE FROM N.A., AND PARTIAL SEQUENCE (MEDIUM FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QUENCE FROM N.A. (LONG FORM AND SHORT FORM)
                                                                                                                                                                                          SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUE-LYMPHOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S., PELLIGRINI I., KELLY P.A.; prolactin-dependent immune cell line (Nb2) expresses a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INE; 90241201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENDOCRINOL. 4:1136-1143(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R., BUCZKO E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95014432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266:20110-20117(1991).
                                                                                                                                                                                                                                                                                                                                   269:26076-26082(1994).
HIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RES. COMMUN. 168:415-422(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSAI-MORRIS C.H., cterization of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
Q62832; Q64274; Q63479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel
                                                           There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HU Z.Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAMMALIA; EUTHERIA;
RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rat ovarian
                                                                                                                                                                                                                                                                           PRODUCED
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                                                                                                                                                                                                                                                                     BY ALTERNATIVE
                                        and.
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PRIR_MOUSE
ID PRIR_M
AC Q08501
DT 01-APR
DT 01-FEB
DT 15-JUL

PRLR_MOUSE Q08501; Q620 01-APR-1990 01-FEB-1995 15-JUL-1998

(REL. 14, CREATED)
(REL. 31, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)

062099;

STANDARD; P15213;

P15212;

PRT;

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Best Local
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SEQUENCE
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VARSPLIC
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VARSPLIC
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DISULFID
DISULFID
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CARBOHYD
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EMBL; U34730;
EMBL; M19304;
EMBL; M74152;
EMBL; U07567;
184 TOFKVFDLYPGOKYLVOTRCKP-----DHGYWSRWSQESSVEMP 222
                                                                                                                                                                                125 SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETELHTNYSLKYKLRWYGQD
                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                  126 RNLTL-EVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00041;
HSSP; P16471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                          242 PDVHVSRVGGLEDQLSVRWY--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 296
                                                                                                                            185 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M57668;
EMBL; M34083;
                                                                                                    66 TTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP
                                                                                                                                                       15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                        TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A2988
                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL;
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLICING
                                                                                                                                                                                                                                                                                555
68599
                                                                                                                                                                                                                                                                                                          ECEPTOR_CYTOKINES_1;
                                                                                                                                                                                                                          13.98;
                                                                                                                                                                                                                                                                                3
                                                                                                                                                                                                               35;
                                                                                                                                                                                                           Score 312; DB 1; 1
Pred. No. 4.3e-18;
5; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN MEDIUM FORM).
MISSING (IN FORM NB2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (BY SIMILARITY). FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                             MISSING (IN SHORT FORM).

KGKSEELISALGCODFPPTSDCEDLLVEFL

TGSPSKYKVDLYLALPGGFQKLDNAGELDY

MEDIUM FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLN (IN SHORT FORM).
MISSING (IN SHORT FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVKQLKDKKTYLWVKWSPPT -> DYRWEVSCHQEALPKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
PROLACTIN RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       بر مر
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT,
                                                                                                                                                                                                                                     Length 610;
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                                                                                                                                                        îi '
                                                                                                                                                                                                          Gaps
                                                                                                     125
                                                                                                                              241
                                                                                                                                                                                 184
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EMBL; M22959
EMBL; M22958
                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                             entities
                                                                                                                                                                                                                                 use
                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SWISS WEBSTER; MEDLINE; 89261824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Changes in prolactin mouse ovary.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               long-form prolactin receptor.";
GENE 134:263-265(1993).
                       CHAIN
                                                                                                                                                                                                                                                                                                                                     ÷
                                                                                PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                   DAVIS J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SASAKI M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENDOCRINOLOGY 133:224-232(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SWISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA;
                                 SIGNAL
                                          ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDERY M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LARKE D.L., LINZER D.I.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 93307149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOORE R.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RODENTIA; SCIUROGNATHI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROLACTIN
                                                                                                                                                                                                                                                                                                                                                                                       Expression of multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning and sequencing of the
                                                                                                                                                                                                                                                                                                                                                                                iver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A. (FORM PRL-R3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A. (FORM PRL-R3).
                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      ENDOCRINOL. 3:674-680(1989).

FUNCTION: THE IS A RECEPTOR FOR THE ANTERIOR PITUITARY PROLACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: THREE FORMS, PRL-R1, PRL-R2 AND PROTEIN.
                                                                                                                                                                                                                                                                                 SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: THREE FORMS; PRL-R1, PRL-R2
SHOWN HERE) ARE PRODUCED BY ALTERNATIVE SPLICING
                                                                                                                                                     L13593; G347842; -. L14811; G293770; -. D10214; G220576; -.
                                                            PF00041; fn3
P16471; 1BP3
                                                                                                                                                                                                  an email to license@isb-sib.ch
                                                                                                                                                                                                                               non-profit
                                                                                                                                                                                                                    and this statement
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                                                                                                                                                                                                            requires a license agreement
                                                    TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JUL-1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                  LINZER D.I.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OKA
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                                          SPLICING
  20
230
230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WEBSTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=MAMMARY GLAND;
                                                                        fn3; 2.
                                                                                                                                                                                                                                                                                BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
  19
608
229
253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FORM PRL-R3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FORM PRL-R3).
                                                                                                                                                                                                                                                                                                                                                                                                                                 (FORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NANDI
                                                                                                                                                                                                                              institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                       forms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MURIDAE; MURINAE;
                                                    GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               s;
                                                                                                                                                                                                                                                                                                                                                                                                                                PRL-R2 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLAND;
                                                                                                                                                                                                                     is not
PROLACTIN RECEPTOR. EXTRACELLULAR (BY S BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               KELLY
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                                                                                                                                                                                                                                                                                                                                                                                                                              PRL-R1).
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                                                 SIGNAL; REPEAT
                                                                                1.
FALSE_NEG.
                                                                                                                                                                                                                                        There
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  during pregnancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAMMALIA;
         (BY SIMILARITY).
                                                                                                                                                                                                                                        are no
                                                                                                                                                                                                                                                                                                                                                                                      receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BANKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                       MEDLINE; 97:
HALABY D., 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC CONFLICT SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
VARSPLIC
VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                           receptor.";
PROTEINS 27:459-468(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                  mammary gland.";
                                                                                                                                                                                                        receptor by molecular
                                                                                                                                                                                                                                                                                                                                                                              ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA; METAZOA; CHORDATA; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                        D-STRUCTURE MODELLING OF 30-228 AEDLINE; 97248733.
                                                                                                                                                                                                                                                                                 TISSUE-MAMMARY GLAND;
MEDLINE; 89184578.
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRLR_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                     Homology modeling
                                                                                                                                                                                                                                                                                                                                                            AGOMORPHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207
                                                                                                                                                                                                                   DERY M., JOLICOEUR C., LEVI-MEYRUEIS C., DUSANTER-FOURT ETRIDOU B., BOUTIN J.M., LESUEUR L., KELLY P.A., DJIANE Identification and sequence analysis of a second form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 LSRLLNTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSR 149
                 FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----DHGYWSRWGQEKSIEIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITDVKTGWFTMEYEIRLKSEEADEWE-IHFTGHQTQFKVFDLYPGQKYLVQTRCKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WKIXIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKETFTCWWNPGSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI
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                                                                                                                                                                  NATL. ACAD.
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558
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               A RECEPTOR FOR THE
                                                                                                                                                                                                      cloning
                                                                     DJIANE J., rabbit prol
                                                                                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                          ORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; ORYCTOLAGUS.
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MISSING (IN PRL-R2),
KGKSEELLSALGCQDFPTSDCE -
PTTEFLCDL (IN PRL-R1),
MISSING (IN PRL-R1),
L -> F (IN REF. 2).
W; AA401E67 CRC32;
                                                                     E'J., MORNON J.P.; prolactin hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                     (PRL-R)
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                86:2112-2116(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                core 307.5;
red. No. 1e-1
Mismatches
                                                                                                                                                                                                      complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  616
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               ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VHNKEQLENYVY (IN PRL-R2).
                                                                                                                                                                                                        DNA
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                                                                                                                                                                                                        of prolactin
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PROLACTIN

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Query Match
Best Local Similarity
77; Conserv
                                                                                                                                                                                                                                                                                            ESULT
                                                                                       GALLUS GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                  SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN; TISSUE-KIDNEY;
MEDLINE; 93075121.
                                                                                                                                                                                                                                                                         CHICK
                                                                                                                                                                                           01-JUN-1994
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                            204594;
                                                                                                                                                                                                                                                        PRLR_CHICK
                                                                                                                                                                                                                                                                                                                                            203
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
 DLINE: 930/5121.
ANAKA M., MAEDA K., OKUBO T., NAKASH
                                                                                                                                                                                                                                                                                                                                                                                                144 KPYLWVKWLPPTLVDVRSGWLTLQYEIRLKPEKAAEWE-THFAGQQTQFKILSLYPGQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                             256
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                                                                                                                                                                                                                         1-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROSITE;
                                                                                                                                                                                                                                                                                                                                                                    FVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                               LSVRWVS--PPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVY 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQ 255
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                                                                                                                                                                                                                                                                                                                                            LVQVRCKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCYFSKKHTSIWTIYIITVNATNOMGSSVSDPRYVDVTYIVEPDPPVNLTL-EVKHPEDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE
                                                                                                                                                                                       (REL.
(REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G165670; -.
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                       ----DHGFWSVWSPESSIQIP 227
                                                                                                                                                               29, CREATED)
29, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
R PRECURSOR (PRL-R) (CPRLP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68840 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 307.5; DB 1;
Pred. No. 1e-17;
8; Mismatches 90;
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; FB6170B1 CRC32;
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   NAKASHIMA K.;
hicken prolactin
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                                                                                                                                                                                                                                                                     196 HSCHI-PKDLALFTPYEIWYEATNRLGSARSDVLTLDVLDVVTTDPPPDV--HVSRVGGL
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                                                                                                                                                                                                                                                                                                     230 PPEKPTIIKCRSPEKETFTCWWKPGLDGG---HPTNYTLLYSKEGEEQVYECPDYRTAGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
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nTOPHYS. RES. COMMUN.
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                                                                                                                  YIIQIHCKP-----DHHGSWSEWSSENYIQIPNDFR
                                                                                                                                                                           KPYLVLTW-SPPPLADVRSGWLTLEYELRLKPEEGEEWETI-FVGQQTQYKMFSLNPGKK 404
                                                                                                                                                                                                        EDQLSVRWVSPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV 309
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35.0%;
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                                                                                                                                                                                                                                                                                                                                                                       ; Score 306; DB 1; Pred. No. 2e-17; 27; Mismatches
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FIBRONECTIN TYPE-III.
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OR FOR THE ANTERIOR PITUITARY HORMONE
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                                                                                                                                                                                                                                                                                                                                                                        96;
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PRIR MEIGA STANDARD Q91094; Q91091; Q91092; 01-NOV-1997 (REL. 35, C 01-NOV-1997 (REL. 35, L

35, CREATED)
35, LAST SEQUENCE UPDATE)

STANDARD;

PRT;

831 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PITTS G.R., YOU S.K., SUBMITTED (MAR-1995) :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-KIDNEY;
ZHOU J.F., ZADWORNY
SUBMITTED (JUN-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) PROLACTIN RECEPTOR PRECURSOR (PRL-R) (TPRLR).
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287 NSCYFDKKHTSFWTVYNITVKATNEMGSNSSDPHYVDVTYIVQPDPPANVTLELKKPINR 346
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                     HSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVVLTDPPPDV--HVSRVGGL
                                                                     PPEKPTITKCRSPEKETFTCWWKPGLDGG---HPTNYTLLYSKEGEEQVYECPDYRTAGP
                                                                                                          PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP 195
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P16471;
                                                                                                                                                    Similarity
77; Conser
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                                                                                                                                                                                                                                            831 AA;
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18₽3.
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                                                                                                                                                                 13.5%;
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TO EMBL/GENBANK/DDBJ DATA BANKS.
A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GUEMENE D., KUNHLI
EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCOPROTEIN; SIGNAL; REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MELEAGRIDIDAE;
                                                                                                                                                                                                                                              Œ;
                                                                                                                                                                 Score 305;
Pred. No. 2
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                                                                                                                                                Mismatches
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                                                                                                                                                2.4e-17;
ches 97;
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RESULT 11
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Query Match
Best Local S
Matches 76
                                                                         CARBOHYD
CARBOHYD
SEQUENCE
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CLARKE L.A., EDERY M., LOUDON A.S., RANDALL V.A., POSTEL-VINAY m.c., KELLY P.A., JABBOUR H.N.;

"Expression of the prolactin receptor gene during the breeding and "expression of the prolactin receptor" gene during the breeding and "expression of the prolactin red deer (Cervus elaphus): evidence for the
                                                                                                                        DOMAIN
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        EMBL; X94953; E218406; -.
PROSITE; PS00241; RECEPTOR_CYTOKINES_1;
PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression of two forms in the testis.";
J. ENDOCRINOL. 146:313-321(1995).
-!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; YEAL
ARTIODACTYLA; RUMINANTIA; PECORA;
                                                                                                                                                                                                                                                                             PFAM; PF00041; fn3; 2.
HSSP; P14787; 1AN3.
RECEPTOR; TRANSMEMBRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRLR_CEREL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DERVUS ELAPHOS (RED DEER).
DIKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROLACTIN RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 EDQLSVRWVSPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV 309
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Similarity 33.0
76; Conservative
                                                                                                                                                                                                                                                                              TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRECURSOR (PRL-R).
                                                                           233
65159 MW;
              13.5%;
                                                                                                                                                                                                                                                                             GLYCOPROTEIN;
36;
Score 303; DB
Pred. No. 2.2e
36; Mismatches
                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
                                                                         POTENTIAL.
POTENTIAL.
721F0366 CRC32;
                                                                                                                                                                   CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                              PROLACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CERVOIDEA; CERVIDAE; CERVINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     581
                                                                                                                                                                                                                                                                             SIGNAL; REPEAT
                DB 1;
?.2e-17;
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                            Length
 Indels
 22;
Gaps
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          Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                 DISULFID
                                                                                                                                                                                                                      TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997
01-NOV-1997
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDITIVE; 93346019.

SCOTT P., KESSLER M.A., SCHULER L.A.;

"Molecular cloning of the bovine prolactin receptor a of prolactin and growth hormone receptor transcripts utero-placental tissues.";

MOL. CELL. ENDOCRINOL. 89:47-58(1992).

-1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PIT
                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L02549; G163618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; E
EUKARYOTA: RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE;
                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189
                                                                                                                                                                                                                                                                                                           ECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROLACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRLR_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSUE-ENDOMETRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 LIHECPDYKTGGPNTCYFSKKHTSIWKIYVITVNAINQMGVSSSDPLYVDVTYIVEPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TQLKIFSLYPGQKYLVQVRCKP-----DHGYWSEWSPESSIQIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANLTL-ELKHPEDRKPYLWIKWEPPTLTDVKSGWFMIQYEIRLKPETAADWE-IHFAAKQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDVHVSRVGGLEDQLSVRWVS--PPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDNTCEEYHTVGPHSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NASLLNGQS-----PPGKPKIIKCRSPGKETFTCWWEPGSDGG--LPTNYTLTYHKEGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit institutions as long
                                                                                                                                                                                                                                                                                                      TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT
     13.4%;
nilarity 31.9%;
Conservative 3
                                                                                              581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                        fn3; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRECURSOR (PRL-R)
                                                                                            ₩;
         38;
     Score 302.5;
Pred. No. 2.4e
98; Mismatches
                                                                                                              POTENTIAL
                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                              FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                      POTENTIAL
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                                                                                                                                                                                                                                                                                         POTENTIA
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                                                                                            COECAOA2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                          removed. Usage by and for commercial ent (See http://www.isb-sib.ch/announce/
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   1.4e-17;
nes 92;
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                                    DB 1;
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                                      Length 581;
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   Indels
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s in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342
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   47;
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Gaps
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DOMAIN
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                   TRANSMEM
DOMAIN
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PROSITE; PS00241;
PROSITE; PS00340;
                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                         PFAM; PF00041;
HSSP; P16471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OREOCHROMIS NILOTICUS (NILE TILAPIA) (TILAPIA NILOTICA).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA; PERCIFORMES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRLR_ORENI
Q91513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANDRA O., SOHM F., DE LUZE A., PRUNET P., EDERY M., KELLY P.A., Expression cloning of a cDNA encoding a fish prolactin receptor ROC. NATL. ACAD. SCI. U.S.A. 92:6037-6041(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDLINE; 95320210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THIS IS A RECEPTOR PROLACTIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKDLTCRWIPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHIVGPHSCHI-PKDLALFIP
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(REL. 35, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
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RECEPTOR_CYTOKINES_2;
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                                                                                                                                                                                                                                             GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342
                                           POTENTIAL.

CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.

BY SIMILARITY.

BY SIMILARITY.
POTENTIAL. POTENTIAL.
                                                                                                                                                                BY SIMILARITY.
PROLACTIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOR THE ANTERIOR PITUITARY HORMONE
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                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.
                                                                                                                                                                                                                                    SIGNAL; REPEAT
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Best Local Similarity
Matches 71; Conser
                                                                                                                                                                                                                                                                                                                 MEDINE: 91011257.

MEDINE: 91011257.

LARSEN A., DAVIS T., CURTIS B.M., GIMPEL S.,

SORENSEN E., MARCH C.J., SMITH C.A.,

SORENSEN E., MARCH C.J., SMITH C.A.,
MEDLINE; 9733132/.
YAMASAKI K., NAITO S., ANAGUCHI
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQU
15-DEC-1998 (REL. 37, LAST ANNO
GRANULOCYTE COLONY STIMULATING
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                    STRUCTURE BY NMR OF 227-334.
                                                                      FUKUNAGA R., 154-
                                                                                                                                         SETO Y , FUKUNAGA R , NAGATA S "Chromosomal gene organization stimulating factor receptor";
                                                                                                                                                                                                          PROC. NATL. ACAD. SCI. U.S.A.
                                                                                                                                                                                                                   "Three different mRNAs factor receptor.";
                                                                                                                                                                                                                                          FUKUNAGA R., SETO Y.,
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CSF3R OR GCSFR.
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                                                                                                 MEDLINE: 92007729.
                                                                                                                                                                                                                                                                                                       A cDNA clone expressed
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                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
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                                                        J. 10:2855-2865(1991).
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172:1559-1570(1990)
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RECEPTOR PRECURSOR (G-CSF-R)
                                                                                                                                                  human granulocyte colony-
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     domain
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                                                                                       SETO Y., NAGATA S.;
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              OTA
   containing
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stimulating factor receptor by molecular modeling
J. BIOL. CHEM. 272:29735-29741(1997).
                                                                                            DOMAIN
                                                                                                                                                                                                                                                 PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                        REPEAT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF THE RECEPTOR.

ONE OR SEVERAL CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL S. IN BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.

THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE GSCFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA. HAT U93 CELLS. THE GSCFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.

ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS, GCSFR-1 (SHOWN UNDER), GCSFR-3 AND GCSFR-4/D7, ARE PROBABLY PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY DIFFER IN THEIR C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: DEFECTS IN CSF3R ARE A CAUSE OF KOSTMANN SYNDROME; ALSO KNOWN AS SEVERE CONGENITAL NEUTROPENIA (SCN).
SIMILARITY: BELONGS TO THE IMMUNOCLOBULIN SUPERFAMILY. CONT
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X55720; G31699; -...

X571484; G240884; -...

M59818; G183047; -...

M59819; G485364; -...

M59820; G183049; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ONE IG-LIKE DOMAIN.
SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS SIMILARITY: CONTAINS 5 THE CYTOKINE FAMILY OF RECEPTORS.
DATABASE: NAME-PROW; NOTE-CD guide CD114 entry:
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd114.htm".
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LAR LOCATION: TYPE I MEMBRANE PROTEIN. THE CLAR LOCATION: TYPE I MEMBRANE PROTEIN. THE CLAR LOCATION: MAY REPRESENT
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                                                          FIBRONECTIN TYPE-III.
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T A SOLUBLE FORM
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P401-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
P401-FUB-1995 (REL. 36, LAST ANNOTATION UPDATE)
P401-1998 (REL. 36, LAST ANNOTATION PRECEPTOR PRECEPTOR PRECEPTOR PRECEPTOR PRECEPTOR PRECEPTOR PRECEPTOR (MOUSE).
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YAMASAKI K., NAITO S., ANI
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; IGCF; 22-OCT-97.
; ICTO; 22-OCT-97.
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SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CYTORINE FAMILY OF RECEPTORS.
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: FOUND IN BONE MARROW.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
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FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN
ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS;
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extracellular domain containing
colony-stimulating factor receptor
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Query Match Best Local S Matches 107

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Score 252.5; | Pred. No. 4.8e | 56; Mismatches

4.8e-

Indels Length

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Search completed: September 17, 1999, 03:10:12 Job time: 292 sec

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                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLel. 01, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHEN J., GRACE A., CHIEN K.R.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
EMBL; AF041845; AAC03531.1; -
PFAM; PF00061; fn3; 4
SEQUENCE 881 AA; 99003 MW; 647E152E CRC32;
       SEQUENCE FROM N.A. MEDLINE; 95286597.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GP130P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                            Eutheria; Primates;
                                                       Eukaryota; Metazoa;
                                                                  Homo sapiens (Human)
                                                                                                                                             Q16354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998
01-MAY-1999
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                                                                            ROLACTIN RECEPTOR (FRAGMENT).
                                                                                                                                                                                                       311 KQVTP--
                                                                                                                                                                                                                                                      256
                                                                                                                                                                                                                                                                             281
                                                                                                                                                                                                                                                                                                     199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ----VLPA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 DPTLLIGS-SLOATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        HTNYSLKYKLRW-----YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL 220
                                                                                                                                                                                                                             AASTPRSERPGPGGGVCEPRGGEPSSGP 365
                                                                                                                                                                                                                                                                         VEDSYDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPT
                                                                                                                                                                                                                                                                                                                         GSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR 280
                                                                                                                                                                                                                                                  PVKTQDWEMVPEEDTASHRDSFTLQDLLPNTVYEVSIRC-
                                                                                                                                                                                                                                                                                                 GIQKSETLTIDPVNIVKPNPPQLSELISSLELPNALKIEWKNPIT---NAFNLKYNIRYR
                                                                                                                                                                                                                                                                                                                                                PTNYTLSH--RWAHFGANYCRGANNSC-----TIHSP-GFQFYIDTTFQVEATNEL 198
                                                                                                                                                                                                                                                                                                                                                                                                                    SRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                              DPGIVHGERPFTAYCVINQTCLREDASRIYWLVKGVKVPETQYEILNQTTSSVTFENLTT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNSPLTCNVMASGHVANTLYGIFFTLGLPPDKPTNLTCIVYNQDNLTCTWDPGR--PTNL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. (TrEMBLrel.
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
                                         Catarrhini; Hominidae;
                                                    Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,6,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               score 355.5; 1; Pred. No. 4.4e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                      PSRGP
                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       881
                                                                                                                                       206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.4e-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                         Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136;
                                                                                                                                                                                                                                                  ----IHKDGHGFWSDWSELK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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Xenopodinae;
                                                     Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
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                                                                                                                                                                                                                                                                          337
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185 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD

SILAGSCLYVGLPPEKPENISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184

-PPEKPKLIKCRSPGKETFTCWWEPGADGG--LPTNYTLTYRKEGETLI 72

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125

Conservative

32;

Indels

22;

Gaps

8

20

SLLNGQS--

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RESULT
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 Query Match
Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                              CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   046561
                                                                                                                                                                                                                                                                                                           Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                  "Long and short forms of the ovine prolactin receptor: cDNA cloning and genomic analysis reveal that the two forms arise by different alternative splicing mechanisms in ruminants and in rodents."; J. Mol. Endocrinol. 19:109-120(1997).
                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TIEMBLIE1. 06, 0
01-JUN-1998 (TIEMBLIE1. 06, 1
01-MAY-1999 (TIEMBLIE1. 10, 1
PROLACTIN RECEPTOR LONG FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 270:13133-
EMBL; S78505; AAB34470:1;
PFAM; PF00041; fn3; 2.
                                                                                                                        SEQUENCE FROM N.A.
BIGNON C., DJIANE J.;
Submitted (JAN-1998) to the
EMBL; AF041257; AAB96795.1;
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 98001468.
BIGNON C., BINART N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Prolactin receptor antagonists that inhibit the growth of breast
                                                                                                             PFAM; PF00041; fn3;
                                                                                                                                                                                                                                                                                                     Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUH G.,
                                                                                                                                                                                                                                        JIANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 YFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 HSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLELAV-EVKQPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLMHECPDYITGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTEFKILSLHPGQK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WELLS J.A.
                                                              25
581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206' AA;
                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270:13133-13137(1995)
                                                            24
581
65235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23950 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --DHGYWSAWSPATFIQIP
          13.6%;
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                                                                                                                                                                                                                                                   ORMANDY C.,
                                                                                                                                   the
                                                               WW.
                                                           POTENTIAL.
PROLACTIN H
6792A7C7
                                                                                                                                                                                                                                                                                                                                                              Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                      EMBL/GenBank/DDBJ
Score 306; DB 6;
Pred. No. 5.8e-19;
2; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 324.5; DB 4;
Pred. No. 3.5e-21;
5; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                   PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D7E57266 CRC32;
                                                                                                                                                                                                                                                SCHULER L.A., KELLY P.A.
                                                                                                                                                                                                                                                                                                                                                                                                               581
                                                            RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342
                                                                                                                                                                                                                                                                                                              ; Vertebrata; Mammalia;
Pecora; Bovoidea; Bovi
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                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                      databases
                     Length 581;
                                                                         LONG
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                                                                         FORM
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                                                                                                                                                                                                                                                                                                               Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
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    Boreferance
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                       Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygi
                                                 01-NOV-1998 (TIEMBLIE1. 08, Created)
01-NOV-1998 (TIEMBLIE1. 08, Last sequence update)
01-MAY-1999 (TIEMBLIE1. 10, Last annotation updat)
PROLACTIN RECEPTOR (FRAGMENT)
                                                                                                                                 093404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endocrinology 138:3187-3194(1997).

EMBL; AF027403; AAB83999.1; -

PFAM; PF00041; fn3; 2.

SEQUENCE 296 AA; 33854 MW; 8B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Fiitheria: Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                 323
                                                                                                                                                                                                       211
                                                                                                                                                                                                                                                               158
                                                                                                                                                                                                                                                                                                                                                                                               151 MKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHI-PKDLALFTP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE, 97375450.
SCHULER L.A., NAGEL
                                                                                                                                                                                                                                                                                          268
                                                                                                                                                                                                                                                                                                                                                 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROLACTIN RECEPTOR SHORT
                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                               41
                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 SRLLNTSTLALALANINGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prolactin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
                                                                                                                                                                                                  ---DHGYWSEWSPESSIQIP
                                                                                                                                                                                                                             GSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                       D-----FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIY 322
                                                                                                                                                                                                                                                                                                                                        YEIWVEATURLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWV--SPPALK 267
                                                                                                                                                                                                                                                              DVKSGWFIIQ-
                                                                                                                                                                                                                                                                                                            YVITVNAINOMGISSSDPLYVHVTYIVEPEPPANLTL-ELKHPEDRKPYLWIKWSPPTMT 157
                                                                                                                                                                                                                                                                                                                                                                    KETFTCWWEPGADGG--LPTNYTLTYHKEGETLIHECPDYKTGGPNSCYFSKKHTSIWKM
                                                                                                                                                                                                                                                                                                                                                                                                                                   SRVVFILLLFLSVSLLNG---QS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKIFNLYPGOKYLVQIRCKP-----DHGYWSEWSPESFIQIP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTL-ELKHPEDRKPYLWIKWSPPTLTDVKSGWFSIQYEIRLKPEKATDWE-THFAPKLTQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 31.9
83; Conservative
                                                                                                                              PRELIMINARY;
Teleostei; Euteleostei;
Labroidei; Cichlidae; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                        -YEIRLKPEKATDWE-THFTLKQTQLKIFNLYPGQKYLVQIRCKP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.
33854·MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.J., GAO J.,
heterogeneity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 302.5; DB 6
Pred. No. 4.9e-19;
8; Mismatches 92
                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8B4 0CCD8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HORSEMAN N.D., I
        ta; Vertebrata; Ac
Acanthopterygii;
                                                                                                                           346 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                ----PPEKPKLVKCRSPG
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L and maternal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                         Actinopterygii;
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Best Local
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Best Local S
Matches 71
                                                                                                                                                                     Matches
                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                           DOUGLAS D.A., SONG J.-H., HC
Submitted (OCT-1997) to the
EMBL; AF029294; AAB88899.1;
PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     046386;
       119
                      274 KYQIRYRVEDSYDWKVYDDYSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEW
                                                                                    219
                                                                                                                                160 PGAHGETFLHTNYSLKYKLRWYGODNTCEEYHTVGPHSCHI-PKDLALFTPYEIWVEATN 218
                                                                                                                                                                                                                                                                                                                      COUGLAS
                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                Mustela vison (American mink).
                                                                                                                                                                                                                                                                                                                                                                                                                                PROLACTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998
01-MAY-1999
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NON_TER 346 346
                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHIRAISHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 TYLIQVRCKP-----DHGFWSEWSSTSYVKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 PEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                           8
                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 WPFLRVSW-EPPHKADTRSGWITLIYELRVKLEDEESEWE-NHAAGQQKMFNIFSLRSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 ---LSVRWVSPPALKDF---LFQAKYQIRYRVED-SVDWKVVDDVSNQTSCRLAGLKPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 CHIPK-DLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQ- 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 PGKPTEITCRSPEKETFTCWWKPGSDGG--LPTTYALYYRKEGSDVVHECPDYHTAGKNS 86
                                                                                                        2 PGEDGG--LPTKYTLTYHKEGETTTHECPDYITSGPNSCYFNKKHTSIWTMYIITINATN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
 QYEIRLKPEKATEWE-THFAGLQTQFKILSLYPGQKYLVQVRCKP---
                                                  EMGSSSSDPRYVTLTYIVEPDPPVNLSL-ELKQPEDKKTYLWIKWYPPTLVDVRSGWLTL
                                                                         RLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVS--PPALKDF---LFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CFFNKNDTLIWYSYNITVVATNALGKTYSDFVDIDVVYIVKPHPPEKLEVT---VMKDQG
                                                                                                                                                                   61;
                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           RECEPTOR (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         8 (TremBirel. 06,
8 (TremBirel. 06,
9 (TremBirel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 AA;
                                                                                                                                                                                                                                    217 AA;
                                                                                                                                                                                                                                                                                                                                                                                       Metazoa;
                                                                                                                                                            10.4%; Score 234.5; DB larity 32.3%; Pred. No. 3.2e-13 Conservative 30; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                    SONG J.-H.,
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; 39203 MW;
                                                                                                                                                                                                                                   217
24850 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.9%;
                                                                                                                                                                                                                                                                                                   HOUDE A., MURPHY B.I
he EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and cortisol
                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 268.5; DB : Pred. No. 5.9e-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nis mossambicus).";
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                   F77A3B9D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1E8A63B9 CRC32;
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                                                                                                                                                                                         DB 6;
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                                                                                                                                                                                                                                                                                                   databases
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-DHGFWSEW
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                                                                                                                                                           Gaps
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                         333
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Best Local S
Matches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-1997) to the EMBL; Y14753; CAA75048.1; ... PFAM; PF00041; fn3; 1. SEQUENCE 198 AA; 22652 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cervus elaphus nelsoni (American elk).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia; i
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                    Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                P79203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation updat
                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOLUBLE PROLACTIN RECEPTOR
                                                                           STRAIN-M22/80; TISSUE-ANTERIOR PITUITARY; TORTONESE D.T., BROOKS J., INGLETON P., M Submitted (JAN-1997) to the EMBL/GenBank/
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                     PROLACTIN RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                        Caprinae; Ovis.
                                               PFAM; PF00041;
                                                                                                                                                                                                                                                                                                                                                                                  189
                                                                                                                                                                                                                                                                                                                                                                                                                297
                                                                                                                                                                                                                                                                                                                                                                                                                                               131 ANLTL-ELKHPEDRKPYLWIKWFPPTLTDVKSGWFMIQYEIRLKPETATDWE-HDDLHPP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 DGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ervinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71
                                                                                                                                                                                                                                                                                                                                                                                                                TSCR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIHECPDYKTGGPNTCYFSKKHTSIWKIYVITVNAINQMGVSSSDPLYVDVTYIVEPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDNTCEEYHTVGPHSCHI-PKDLALFTPYEIWVEAINRLGSARSDVLILDVLDVVTTDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NASLLNGQS-----PPGKPKIIKCRSPGKETFTCWWEPGSDGG--LPTNYTLTYHKEGET
                                                                                                                                                                                                                                                                                                                                                                                  TSSR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDVHVSRVGGLEDQLSVRWVS--PPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62; Conservative
                                                            d (JAN-1997) to the EMBL/GenBank/DDBJ .0578; CAA71597.1; -.
 335 AA;
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                               fn3; 1
 335
38326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22652 MW;
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 WW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
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Pred. No. 6.4
                                                                                                                                                                                                                                                                                                     PRT;
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 88A05AB1 CRC32;
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                                                                                                                                                                                                                                                                                                     335
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                                                                             MCNEILLY A.S.;
k/DDBJ databases
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                                                                                                                                                                        Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Matches 58; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
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01-NOV-1998 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAEDA M., YAGUCHI N., HANYUU C., NAKATA Y., ON
KOJIMA T., HASEGAWA M., KIKUCHI Y., NOMURA H.;
"Mouse homolog of human cillary neurotrophic f
submitted (MAY-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; C
Eutheria; Rodentia; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 088507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAEDA M., YAGUCHI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CILIARY NEUROTROPHIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 AASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 ARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278
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                                                                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                                                                               87 PSELSRLLNTSTLALALANLNGSRQQSGDNLVCHARDGSILAGS-CLYVGLPPEKPFNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                               30 CYLGYPRGGSGAHTAYISPQDPTLLIGSSLQATCSIHGDTPGATAE---GLYWTLNGRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                              LSVRWVSPPALKD-FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQV
                                                                                                                                           CHIPKDLALFT - - PYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQ 255
                                                                                                                                                                                                                                                  CWSRNM-KDLTCRW-----TPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS
LEVTWQTPSTWPDPESFPLKFFLRYRPLILDQWQHV-ELSDGTAHTITDAYAGKEYIIQV
                                                                                               CHI-RYMHLFSTIKYKVSISVSNALGH-NTTAITFDEFTIVKPDPPENVVARPVPSNPRR
                                                                                                                                                                                               CRSNTYPKGFYCSWHLPTPTYIPNTFNVTVLHGSKIM------VCEKDPAL-KNR
                                                                                                                                                                                                                                                                                                 APD---LINGSQLILRSLELGHSGLYA-----CFHRDSWHLRHQVLLHVGLPPREPV-LS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.0%;
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Last annotation update)
RECEPTOR ALPHA PRECURSOR
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8; Mismatches 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 226; DB 11;
Pred. No. 3.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALPHA. 9A40FE12 CRC32;
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CILIARY NEUROTROPHIC
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Mus.
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Best Local Similarity
Matches 84; Conser
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GATELY M.K., GUBLER U.;
Submitted (JUL-1996) to the
EMBL; U644198; ABA36675.1; -
PFAM; PF00041; fn3; 3.
SEQUENCE 862 AA; 97134 M
SEQUENCE FROM N.A
                                             Mus musculus (Mouse).
                                                                    01-MAY-1997 (Tremblrel.
01-MAY-1997 (Tremblrel.
01-NOV-1998 (Tremblrel.
INTERLEUKIN 12 RECEPTOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                              300
                                                                                                                                                                                                                 321 IYGSKKAGIWSEWSHPTAASTPRSERPG
                                                                                                                                                                                                                                                                     261
                                                                                                                                                                                                                                                                                              198
                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                              141
                                                                                                                                                                                                                                                                                                                                                    154 LTCRWTPGAHGETFLHTNYSLKY----KLRWYGQ--DNTCEEYHTVG------PHSCHI 200
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1-MAY-1997 (TIEMBLIEL
1-NOV-1998 (TIEMBLIEL
L-12 RECEPTOR BETA2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUENCE FROM N.A
                                                                                                                                                                                                                                                            VSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFG
                                                                                                                                                                                                                                                                                                            PKDLALFTPYEIWYEATNRLGSARSDYLTLDYLDVVTTDPPPDVHVSRVGGLEDQLSVRW 260
                                                                                                                                                                                                                                                                                                                                    VACTWERGR--DTHLYTEYTLQLSGPKNLTWQKQCKDIYC-DYLDFGINLTPESPESNFT 197
                                                                                                                                                                                                                                                                                                                                                                                                          NTSTLALLANLNGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPENISCWSRNMK-D 153
                                                                                                                                                                                                                                                                                             AK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                 ILLGSTVNITCSL-----KPRQGCFHYSRRNKLILYKFDRRINFHHGHSLNSQVTGLPL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLIGSSLOATCSIHGDTPGATAEGLYWTL-----
                                                                                                                                                                                                                                                                                                                                                                                           GTTLFVCKLACINSDEIQ
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                     Rodentia;
                                                                                                                                                                                          -KGSWSDWSESLRAQTPEEEPTG
                                                                                                                                                                                                                                     RDEGLVLLNRLRYRPSNSRLWNMVNVTKAKGRHDLLDLKPFTEYEFQI-SSKLH
                                                                                                                                PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.7%;
ilarity 25.6%;
Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DNEIGTWSDWSVAAHATPWTEEPRHLTTEAQAPETTTSTTSSLAPPPTTKI
                                                                                                                                                                                                                                                                                     -VTAVNSLGSSSSLPSTFTFLDIVRPLPPWDIRIKFQKASVSRCTLYW
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97134 MW;
                     Chordata; Craniata;
Sciurognathi; Murida
                                Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MINETTI L.J.,
                                                                03, Created)
03, Last sequence update)
08, Last annotation update)
, BETA 2 (IL-12 RECEPTOR BETA2).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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Pred. No. 6.1e-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                    niata; Vertebrata;
Muridae; Murinae;
                                                                                                                                                                                          323
                                                                                                                                                                                                                  348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NGRRLPSELSRL-L
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                  Mammalia;
Mus.
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WOOD
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Best Local
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                            MINVIELLE S
Submitted (NOV-1994) to the EMBL; U32324; AAB36492.1; -.
                                                                                                                                                      CHEREL M., SOREL M., LEBEAU B., DUBOIS S MINVIELLE S., JACQUES Y.;
"Molecular cloning of two isoforms of a hematopoietic cytokine interleukin-11.";
Blood 86:2534-2540(1995).
                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last ann
INTERLEUKIN-11 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                     Q16542
Q16542;
                                                        ISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                     EDLINE; 95399754
                                                                                                                                                                                                                                                                                             Sutheria; Primates;
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-1996) to the EMBL; U64199; AAB36676.1; -. MGD; MGI:1270861; IL12RB2.
                                                                    EQUENCE OF 3-390 FROM N.A.
                                                                                                                   AN LEUVEN F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 WSEWSHPTAASTPRSERPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 AKYQIRYRVEDSYDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSK---KAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 RVTAINDLGNSSSLPHTFTFLDIVIPLPPWDIRINFLNASGSRGTLQW-----EDEGQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 K--VTYLKTNYTLQLS----GPNNLTCQKQCFSDNRQNCNRLDLGINLSPDLA-ESRFIV
                                                                                                    ubmitted (SEP-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 ANINGSROOSGDNL-VCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMK-DLTCRWTPG 161
                                                                                                                                                                                                                                                               QUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 CKLNCSNSQKKPPVPVC
                                                                                                                   QUENCE FROM N.A.
N LEUVEN F., STAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WSNWSESLRTRTPEEEPVG
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                                                                                                                                                                                                                                                                                                                                                                                                     2; Q14626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WVEATHRIGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                          SOREL M.,
                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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ც:
                                                                                                                                                                                                                                                                                       Chordata; Craniata; Ven
Catarrhini; Hominidae;
                                       DUBOIS S.,
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25.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MINETTI L.J.,
                                                                                                  HILLIKER C.,
the EMBL/Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348
          EMBL/GenBank/DDBJ databases
                                                                                                 LIKER C., MIYAKE Y
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59;
                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 215.5;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GVEISVGVAPEPPQNISCVQEGENGTVACSWNSG
                                         LEBEAU
                                                                                                                                                                                                                 DUBOIS S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9B90EB47
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                                       в.
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                                                                                                                                                                                                                                                                                                     Vertebrata; Mammalia;
                                                                                                                                                                                    receptor
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                                      MOREAU J.,
                                                                                                                                                                                                                 MOREAU
                                                                                                                                                                                                                                                                                            Homo
                                                                                                 Y., GOSSLER.
BJ databases.
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                                                                                                                                                                                      for
                                                                                                                                                                                                                 J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -HIPKOLALFTPYEI
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                                                                                                                                                                                    the human
                                       JACQUES
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1)
(IL-11RALPHA) (ILLIRAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                 STRAIN-BALD/C, AND C57BL/6; TISSUE-EMBRYO; NEUHAUS H., BETENHAUSEN B., BILINSKI P., GUENET J.L., GOSSLER A.; Dev. Biol. 166:521-542(1994).
                                                                                                                                GOUGH N.M. BEGLEY C.G., METCALF D., "Cloning of a murine II-11 receptor & gpl30 for high affinity binding and & EMBO J. 13:4765-4775(1994).
                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-C57BL/6 X CBA; TISSUE-LIVER;
MEDLINE; 95045367.
HILTON D.J., HILTON A.A., RAICEVIC
             SEQUENCE FROM N.A. STRAIN-BALB/C, ANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
  GOSSLER A.;
                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                            Q64385
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368
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                                                                                                                                                                                                                                                                                             LIIRAI OR ILIIRA OR ETL2 OR ET12/IL11 REC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 ADYENFSCTWSPSQ--ISGLPTRYLTSYRKKTVLGADSQRRSPSTGPWPC--PQDPLGAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAVISPODPTLLI-------GSSLQATCSIHGDTPGATA-EGLYWTLNG--RRLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRWVSP---PALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLK-----PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDSGLGHELVLAQADSTDEGT-----YICQTLDGALGGTVTLQLGYPPARPV-VSCQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELSRLINTSTLALAULNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TALVSASSPCPQAWGPPGVQYGQPGRSVKLCC-----PGVTAGDPVSWFRDGEPKLLQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEIP---AWGQLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPHAVRVSARDF ----- LDAGTWSTWS - PEA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASWTYPASWPCQPHFLL--KFRLQYRPAQHPAWSTVEP-----AGLEEVITDAVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LALFTPYEIWVEATNRLGSARSDYLTLDYLDVVTTDPPPDVHVSRVGGLEDQLS
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PF00047;
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U32323;
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                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                 HILTON A.A.,
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AAB36491.1;
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               AND C57BL/6;
                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45222
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                                                                                                                                                                                    RAICEVIC A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 209.5; DB 4;
Pred. No. 1.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                             ptor alpha-chain;
and signal trans
                                                                                                                                                                       NICOLA N.A.,
                                                                                                                                                                                                                                                                                                                                                                                         432 AA
                                                                                                                                                                                     RAKAR S., HARRISON-SMITH
                                                                               SIMON-CHAZOTTES D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138;
                                                                                                                                                           requirement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----WGTPSTGTIP
                                                                                                                                                                       WILLSON T.A.
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Mus.
                                                                                                                                                                                                                                                                                                                        (ETL2)
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Best Local S
Matches 94
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CARBOHYD
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TRANSMEM
DOMAIN
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EMBL; U14412; AAA53248
EMBL; X94162; CAA63873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-1995)
[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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GOSSLER A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 97129000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS
                                                                                                                                                  232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Two differentially expressed interleukin-11 receptor genes in
   312
                             347
                                                          270
                                                                                        289
                                                                                                                   212
                                                                                                                                                                              155
                                                                                                                                                                                                           183
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SUBUNIT: HETERODINER OF AN ALPHA AND A BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONTAINS ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN BINDS TO IL-11 WITH LOW AFFINITY, BUT DOES NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ğ
                                                                                                                                                                                                                                                                                                                                                                                       GPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIH
                           PGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKH 380
                                                          TVEPIGLEEVITDAVAGLP ---- HAVRVSARDF ----- LDAGTWSAWS - PEA --
                                                                                      VVDDVSNQ--TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSER
                                                                                                                  LQSILRPDPPQGLRVESVPGYPRRLHASWTYPASWRRQPHFLL--KFRLQYRPAQHPAWS
                                                                                                                                               VLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALK---DFLFQAKYQIRYRVEDSVDWK
                                                                                                                                                                              GAESQRESPSTGPWPC--PQDPLEASRCVVHGAEFWSEYRINVTEVNPLG-ASTCLLDVR
                                                                                                                                                                                                 QDNTCEEYHTVGPHSCHIPKD-------LALFTPYEIWVEATNRLGSARSDVLTLD
                                                                                                                                                                                                                                       DGVSGGMVTLKLGFPPARP-EVSCQAVDYENFSCTWSPGQ--VSGLPTRYLTSYRKKTLP
                                                                                                                                                                                                                                                                   DGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYG
                                                                                                                                                                                                                                                                                                --TP-----VSWFRDGD-----SRLLQGPDSGLGHRLVLAQVDSPDE---GTYVCQTL
                                                                                                                                                                                                                                                                                                                          GDTPGATAEGLYWTLNGRRLPSELSRLLN--TSTLA--LALANLNGSRQQSGDNLVCHAR
                                                                                                                                                                                                                                                                                                                                                            GPPGVQYGQPGR-----PVMLCCPGVSAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISSUE SPECIFICITY: WIDELY EXPRESSED.
IMILARITY: BELONGS TO THE IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 23.9
94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. 320:359-363(1996)
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WGTPSTGPLQDEIPD -- - WSQGH
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 208.5; DB 1
Pred. No. 1.5e-10;
1; Mismatches 136
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Query Match
Best Local
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CARBOHYD
CONFLICT
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DOMAIN
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T. Biol. Chem. 271:13754-13761(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 02, Last sequence update)
INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2 PRECURSOR (IL11RA2)
IL1-11RBETA, (INTERLEUKIN-11 RECEPTOR BETA CHAIN)
LL11RA2 OR IL-11RBETA.
Us musculus (Monse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRAIN-CD1; TISSUE-TESTIS;
EDLINE; 97129000.
SILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1997
01-FEB-1997
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Sutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DBB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.G.; Identification of a second murine interleukin-11 receptor lpha-chain gene (IL11Ra2) with a restricted pattern of expendings 40:387-394(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRAIN=CD-1; TISSUE=TESTIS; EDLINE; 97230451.
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EDLINE; 96278810.
                                                                      Match 8.9%;
Local Similarity 24.6%;
es 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: WIDELY EXPRESSED.
SIMILARITY: BELONGS TO THE IMMUNOCLOBULIN SUPERFAMILY.
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                           GPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIH 66
   GPPGVQYGQPGR---
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                                                                                                                                                                   Ψ.
                                                                        49;
                                                                  Score 201; DB 11;
Pred. No. 7e-10;
9; Mismatches 148;
                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
POTENTIAL.
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-> L (IN CAA63872).
C4FD7DEC CRC32;
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320 LQDEIPDWSQGHGQQLEAVVAQEDSLAPARPSLQ
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                                        343 -RSERP----GPGGGVCEPRGGEPSSGPVRRELK 371
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                                                                           TVEPIGLEEVITDTVAGLP----HAVRVSARDF-----LDAGTWSAWS-PEAWGTPSTGL 319
                                                                                                                                                                                            VLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALK---DFLFQAKYQIRYRVEDSVDWK 288
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Search completed: September 16, 1999, 20:40:05 Job time: 5556 sec

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Clone 25-1 encoded Human GCSF recepto

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Best Local
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Claim 15: Page 84-87; 182pp; English.
The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6.
The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6.
Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang J;
WPI; 98-260970/23.
N-PSDB; V27141.
New 1solated haemopoletin
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY
(DZIE/) DZIEGLEWSKA H E.
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Haemopoietin receptor; cell
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  361 PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGAA
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ilarity 100.0%;
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3h A, Nicola NA, Rakar S, Willson
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proliferation; cell different
neuronal proliferation; drug
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Pred. No. 1.1
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1.1e-191;
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Result

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Match

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SUMMARIES

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Scoring table: Sequence Perfect score:

BLOSUM62

188963 seqs, 23686106 residues

US-09-037-657-15 2317 1 MPAGRPGPVAOSARR

MPAGRPGPVAQSARRPPRPL...

.....NQDEGILPSGRRGAARGPAG

425

OM protein .

protein search, using sw

model

Copyright

GenCore version 4.5 (c) 1993 - 1998 Compugen Ltd

September 17, 1999, 03:08:12;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding U4 haematopoietin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease SC laim 9; Pages 26-27; 38pp; English.

This is the amino acid sequence of the murine U4 protein from the haematopoietin receptor superfamily, used in the method of the cresponse. Transformed mammalian cells proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and a stissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune cancer, and altergy).

Sequence 425 AA;
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15-JAN-1998; U00334.
16-JAN-1997; US-784863.
(GEMY ) GENETICS INST IN
COllins M, Donaldson DD,
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  PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGAA
                                                                                                                                            LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE
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                               LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE
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2 sequence of the murine U4 protein.
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Pred. No. 2.3e
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fy; cell differentiation;
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                                                                                                                                        The present sequence represents a protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
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anance factor; thyroid; heart;
ac pathology; heart enlargemen
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                          PPDVHYSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCR
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Pred. No. 3.3e
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3.3e-189;
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-1996; AU-002246.
(AMRA-) AWRAD OPERATIONS PTY LTD.
(ZIEF) DZIEGLEWSKA H E.
Alexander W. Fabri L. Farley A. Hilton DJ. Kikuchi Y.
Alexander W. Fabri L. Farley A. Hilton DJ. Kikuchi Y.
Kojima T. Maeda M. Nash A. Nicola NA. Rakar S. Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated haemopoietin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; V27140
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WPI; 98-260970/23.
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11-SEP-1997;
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MO9811225-A2.
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l; therapeutic;
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Pred. No. 6.3e-184;
2; Mismatches 0;
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                                                                                                                                                                                                                             Best Local S
Matches 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        maintenance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Zcytor5
Zcytor5; cyto
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WO9849307-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiac pathology;
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 66-67; 55pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New mammalian
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13-FEB-1998; US-074
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YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDP
                                                                                        ARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW
                                                                                                    ARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRW
                                                                                                                                   ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH
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Similarity 94.68;
O1; Conservative
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L. Foster DC, Gilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytokinin-like receptor; down-regulation; nce factor; thyroid; heart; skeletal muscl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-023890
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytokinin-like receptor 2cytor5 - useful for, e.g.
ng 2cytor5 natural ligands or detecting cardiotrophin-1
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                                                                                                                                                                                                                             Score 2172.5;
Pred. No. 2.9e
6; Mismatches
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e; cardiotrophin-1;
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CC This is the amino acid sequence of the human U4 protein from the CC haematopoietin receptor superfamily used in the method of the CC invention for the modulation of cell proliferation, or the immune CC response. Transformed mammalian cells are used to produce recombinant CC U4 protein. The U4 protein is used to screen for specific binding CC agents, raise antibodies. It is also used as reagents for assays and CC as tissue markers for isolation of cognate ligands and receptors, and CC cell differentiation, and the immune system (e.g. for treating immune CC deficiency, inherited or the result of infection, autoimmune diseases, Sc cancer, and allergy).

Sequence 408 AA;
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Best Local Similarity
Matches 390; Conser
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Amino acid sequence of the human U4 p
Human; U4 protein; haematopoietin rec
cell proliferation; immune response;
autoimmune disease; cancer; allergy.
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16-JAN-1997;
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     QLSVRWVSPPALKDFLFQAKYQIRYRVEDS
                 QLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQV
                                                                                  PHSCHIPKDLALFTPYEIWVEATNRLGSARSDYLTLDYLDYVTTDPPPDVHYSRYGGLED
                                                                                                                                                                                                 EGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYV
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                                                                        PHSCHIPKDLALFTP.
                                                                                                                                   GLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVG
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                                                                 /EATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLED
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Pred. No. 1.8e-174;
5; Mismatches 12;
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VDWKVVDDVSNQTSCRLAGLKPGTVYFVQV
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ody; cell differentiation;
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01-MAY-1998; U08865.

13-FEB-1998; US-074721.

01-MAY-1997; US-045287.

01-MAY-1997; US-850030.

13-FEB-1998; US-023890.
thyroid, heart, and skeletal muscle for example to the control of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Ecytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Ecytor5 ligands. A probe comprising Ecytor5 DNA or RNA can be used to determine the presence and integrity of the Ecytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Ecytor5 and therapeutically to modify Ecytor5 ligand effects.
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Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
                                                                                                                                                                                                                                                           The present sequence represents a 2cytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effects of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mammalian cytokinin-like receptor 20 down-regulating Zcytor5 natural ligands
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 83-84; 55pp; English
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ds or detecting cardiotrophin-1
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TPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK
                        VEDSVDWKVVDDVSNOTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS
                                                                                            GSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR
                                                                                                                            GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL
                                                                                                                                           GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL
                                                                                                                                                                                               LALANINGSRQOSGDNIVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTP
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                                                                             GSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR
                                                                                                                                                                                 LALANINGSROOSGDNIVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTP
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                    90.5%;
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                                                                                                                                                                                                                                                                                       Score 2097; DB 1;
Pred. No. 8.1e-173;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                               385;
                                                                                                                                                                                                                                                                                     Gaps
 400
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mammalian cytokinin-like
down-regulating Zcytor5 natur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; V70895
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Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiac pathology; heart enlargement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 99-034662/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )1-MAY-1997;
.3-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    illelic varaint of human Zcytor5.
cytor5; cytokinin-like receptor; di
aintenance factor; thyroid; heart;
 301
                                 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aim 1; Page 71-72; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                             MPAGRPGPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQ 60
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                              ATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCH
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                                                                                                                                                                                                                             ATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALANLNGSRQRSGDNLVCH
                                                                                                                                                                                                                                                                                           MPAGRRGPAAQSARRPP-PLLPL---LLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLL
                                                                                                                                                                                                                                                                                                                                                          Similarity 94.8
86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            425 AA;
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US-045287.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 425
                                                                                                                                                                                                                                                                                                                                                                           90.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -like receptor Zcytor5 - useful for, e.g.
natural ligands or detecting cardiotrophin-1
                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                         Score 2094; DB 1;
Pred. No. 1.7e-172
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                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 373
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Lok S, Pre
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cardiac pathology; heart enlargement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New mammalian cytokinin-like down-regulating zcytor5 natur
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maintenance factor; thyroid; heart;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 80-81; 55pp;
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                                                                                                                                                                                                                                                           38 GSGAHTAVISPODPTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTS
                                                                                                                                                                                                                                                                                            Local Similarity es 373; Conserv
                                                                                                                                                                                                                            RYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPT 337
                                        NRLGSARSDYLTLDILDVVTTDPPPEVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQI
                                                       NRIGSARSDVLTLDVVLTVDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQI
                                                                                                      WTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEAT
                                                                                                                      WTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWYEAT
                                                                                                                                                                  TLALALANLNGSRORSGDNLVCHARDGSILAGSCLYYGLPPEKPVNISCWSKNMKDLTCR
                                                                                                                                                                               TLALALANINGSRQQSGDNIVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99-034662/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ZYMOGENETICS INC.
RL, Foster DC, Gilbert
Presnell SR, Whitmore
                                                                                                                                                                                                                                                                                                                                                                      388 AA;
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                       88.5%;
96.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             natural ligands
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                                                                                                                                                                                                                                                                                            6;
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Pred. No. 7.56
6; Mismatches
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/.5e-169;
8;
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cardiotrophin-1
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                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 370; Conser
                                                                                                                                                                                                                                                                                                                                           The present sequence represents a Zcytor5 variant protein. Zcytor5 is a Cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down-regulating Zcytor5 natural ligands or detecting cardiotrophin-l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZYMO ) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zcytor5; cytokinin-like receptor; down-regulation; g
maintenance factor; thyroid; heart; skeletal muscle;
cardiac pathology; heart enlargement; Zcytor5 ligand
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Zcytor5; cytok
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13-FEB-1998;
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  VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS
                                            GSARSDYLTLDYLDYYTTDPPPDYHYSRYGGLEDQLSYRWYSPPALKDFLFQAKYQIRYR
                                                                                     GAHGETTLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWYEATNRL
                                                                                                     GAHGETFLHINYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL
                                                                                                                                                              LALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPERPENISCWSRNMKDLTCRWTP
                                                                                                                                                                                                    AHTAVISPQDPTLLIGSSLLATCSVHGDPPGATAEGLYWTLXGRRLPPELSRVLNASTLA
                                                                                                                                                                                                                              AHTAVISPODPTLLIGSSLOATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLA 100
                             GSARSDYLTLDILDVYTTDPPPEVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR
                                                                                                                                               LALANLNGSRORSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTP
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nilarity 96.4%;
Conservative
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US-023890.
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US-074721.
US-045287.
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                                                                                                                                                                                                                                                             Score 2035; In Pred. No. 1.866; Mismatches
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.8e-167;
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                                                                                                                                                                                                                                                                                        Length 385;
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RYRVEDSVDWXVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPT

277 240 337

NRLGSARSDVLTLDVVLTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQI

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                                                                                                                            Query Match
Best Local Sin
Matches 359;
                                                                                                                                                                                                                                                                                                                                                            is a cytokinin-like receptor. Soluble Zcytor5 wariant protein. Zcytor5 down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
                                                                                                                                                                                                                                                                                                                                                     Lok S, Presnell SR WPI; 99-034662/03.
                                                                                                                                                                                                                                                                                               Claim 1; Page 81-82; 55pp; Engli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          maintenance factor;
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                                        61 TLALALANLNGSRORSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCR
                                                                                 98 TLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCR
            WTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHI©KDLALFTPYEIWVEAT
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 WTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEAT
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                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathology; heart
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                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                cytokinin-like receptor Zong Zcytor5 natural ligands
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97.0%;
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Pred. No. 1.5e
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L.5e-162;
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Juman Zcytor5 variant.

Zcytor5; cytokinin-like receptor; down-regulation; gro
Zcytor5; cytokinin-like receptor; down-regulation; gro
Zcytor5; cytor5 variant.

maintenance factor; thyroid; heart; skeletal muscle; c
maintenance factor; thyroid; heart enlargement; Zcytor5 ligand;
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Adams RL, Foster DC, Gilbert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ok S, Presnell SR, Whitmore
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                                                                                                                                                                                                                            241 RYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPT
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les 357; Conservative
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                    VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS
                                                                                            GSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDELFQAKYQIRYR
                                                                                                                                                    GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL
                                                                                                                                                                                                                                                                                                          AHTAVISPODPTLLIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLA
                                                                          GSARSDYLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR
VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                      84.7%;
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Pred. No. 2.9e-16:
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Matches 356
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Zcytor5; cytokinin-like receptor; down-regulation; maintenance factor; thyroid; heart; skeletal muscle maintenance factor; thyroid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 87-88; 55pp;
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Lok S, Presnell S
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             VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS
                                                                                                        GAHGETFLHINYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL
                                                                                                                                 GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL
                                                                                                                                                                                                                                                                     356;
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Pred. No. 3.5e
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1.5e-161;
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r5 ligand;
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Best Local Similarity
Matches 355; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 99-034662/03.

New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
down-regulating Zcytor5 natural ligands or detecting cardiotrophin-l
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Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
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01-MAY-1997; US-850030
13-FEB-1998; US-023890
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                                      241
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TPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK 400
                                                                                                                                             LALANLNGSRQQSGDNLYCHARDGSILAGSCLYYGLPPEKPFNISCWSRNMXDLTGRWTP 160
                            VEDSVDWKVVDDVSNOTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS
                                             VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS
                                                                                     GARSDYUTLDIUTTTDPPPDYHYSRYGGLEDQLSYRWYSPPALKDFLFQAKYQIRYR
                                                                                                      GSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR
                                                                                                                                                                                                                                                              AHTAVISPODPTILIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLA
                                                                                                                                                                                                         SHKTRNQ 367
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US-045287.
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Pred. No. 4
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4.3e-161;
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e; cardiotrophin-1;
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13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a Zcytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New mammalian cytokinin-like receptor down-regulating Zcytor5 natural ligano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 99-034662/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (2YMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T,
Lok S, Presnell SR, Whitmore TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 98-99; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zcytor5; cytokinin-like receptor; down-regulation; growth maintenance factor; thyroid; heart; skeletal muscle; cardi
                                                241
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TPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWWQX
                                                                                                            GSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR 280
                                                       VEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS
                                                                                                                                                   GAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL
                                                                                             GSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR
                                                                                                                                                                  GAHGETFLHTNYSLKYKLRWYGODNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL
                                                                                                                                                                                                       LALANLNGSRORSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTP
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                                         VEDSVDWKVVDDVSNQTSCRIAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAS
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t; Zcytor5 ligand;
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ds or detecting
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5.2e-161;
les 6;
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cting cardiotrophin-l
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Db 301 TPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQK 360

Qy 401 SHKTRNQ 407
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Db 361 SHKTRNQ 367

Search completed: September 17, 1999, 03:08:13 Job time: 304 sec

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

September 16, 1999, 20:41:06 ; Search time 53.94 Seconds (without alignments)
77.754 Million cell updates/sec

Title: Perfect score: Sequence: US-09-037-657-15 2317

1 MPAGRPGPYAQSARRPPRPL.....NQDEGILPSGRRGAARGPAG 425

Scoring table: BLOSUM62

Searched: 106577 seqs, 9868381 residues

Database :

Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

4: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID 1																																											
Outery Match Length DB ID Description 122 Match Length DB ID Description 12329 14.2 708 1 US-07-797-556-2 124.2 708 3 PCT-US95-0530-2 14.5 11.0 863 1 US-07-923-976-4 15. 11.0 863 1 US-07-923-976-6 15. 10.9 837 1 US-07-923-976-2 16. 10.9 837 1 US-07-923-976-2 17. 10.9 837 1 US-07-865-878A-4 18. 10.9 837 1 US-08-449-329-2 18. 10.9 8.3 633 632 1 US-08-849-329-2 18. 10.9 915-495-2 18. 10.9 915-4	39	38	37	36	i U	34		ى د د	<u>ا</u> ا	30	2 2) k) _~) K	2 2	2) L	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	თ	υı	4	ω	N	_	200	Result		
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us-07-960-389-2	US-08-850-293-5	US-08-609-572-2	US-08-588-190-3	US-08-445-640-35	US-08-588-526-3
Sequence 2, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 35, Appl	Sequence 3, Appli

ALIGNMENTS

. 8 Ş 8 멹 밁 Ş 283 DSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAA 339 223 ARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWYSPPALKDFLFQAKYQIRYRVE 282 151 --ETHLETNFTLKSEWATHKFADCKAKRDT--PTSCTVDYSTVYFVNIEVWVEAENALGK 206 163 HGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGS 222 103 LANLNGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGA 162 91 FTDIASLNIQLTCNILTFGQLEQNVYGITIISGLPPEKPKNLSCIVNEGKKMRCEWDGGR 150 31 ISPESPVVQLHSNETAVCVLKEKCMDYEHVNANYIVWKTNHFTIPKEQYTIINRTASSVT 90 VTSDHINFDPVYKVKPNPPHNLSVINSEELSSILKLTWTN-PSIKSVII-LKYNIQYRTK 264 STLALA 102 8; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 VSPPALKD-FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 RLLNTSTLALALANLNGSRQOSGDNLVCHARDGSILAGS-CLXYGLPPEKPFNISCWSRN 150
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ELEPHONE: 212 790-9090
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                                        MPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
APPLICATION NUMBER:
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           ARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
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                                                                                                                                        New York
                                                                                                                                                                       ): Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                   Yancopoulos, George D.
PRITION: The Ciliary Neurotrophic Factor Receptor
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                                                                                                                                                                                                                                                                                     Stephen P.
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                                                                                       TREET:
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, MOLECULE TYPE: protein US-08-449-329-2
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Best Local Similarity
Matches 96; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 DLALFT--PYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRW 260
                                                                                                                                                                                                                                                                                                                                                                                                                    168 YMHLFSTIKYKVSISVSNALGH-NATAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 AHTAVI-----SPODPTLL----IGSSLOATCSIHGDTPGATAEGLYWTLNGRRLPSELS 91
                                                                                                                                                                                                         338 GELGSG 343
                                                                                                                                                                                                                                                                        284 ----DNEIGTWSDWSVAAHATPWTEEDRHLTTEAQAAETTTSTTSSLAPPPTTKICDP-- 338
                                                                                                                                                                                                                                                                                                              320 GIYGSKKAGIWSEWS----
                                                                                                                                                                                                                                                                                                                                                                              261 VSPPALKD-FLEQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 -LLNGSQLV----LHGLELGHSGLYACFHRDSWHLRHQVLLHVGLPPREPV-LSCRSNT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 AAAAVVYAORHSPQEAPHVOYERLGSDVTLPCGTANWDAAVT----WRVNGTDLAPD-- 68
                                                                                                                                                                                                                                         359 GEPSSG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLLNTSTLALANINGSROOSGDNLVCHARDGSILAGS-CLYVGLPPEKPFNISCWSRN 150
                                                                                                                                                                                                                                                                                                                                               QTPSTWPDPESFFLKFFLRYRPLILDQWQHV-ELSDGTAHTITDAYAGKEYIIQVAAK--
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                                                                                 INFORMATION:
                                                                                                                    Application US/08445073
INVENTION:
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                                                Squinto, Stephen P.
                                  Furth, Mark E
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 The Ciliary Neurotrophic Factor Receptor
                       George
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 -LINGSQLV-----LHGLELGHSGLYACFHRDSWHLRHQVLLHVGLPPREPV-LSCRSNT 120
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                                                                                                                                                                                                                         GELGSG 343
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ANY: Yancopoulos, George D.
PINVENTION: The Cillary Neurotrophic Factor Receptor OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MMUNICATION INFORMATION:
PHONE: 212 790-9090
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                                                                                                                          Application PC/TUS9103896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 amino acids
                                                 Squinto, Stephen P. Furth, Mark E.
                                                                                            Davis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-1991
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                                                                                        Samuel
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26.2%;
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US-08-685-118-2

Sequence 2, Patent No.

ication US/08685118

PPLICANT:

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Ulrich A David H RECEPTORS FOR HUMAN IL-12

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Best Local S
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338 GELGSG 343
                                                                                                                                        227 QTPSTWPDPESFPLKFFLRYRPLILDQWQHV-ELSDGTAHTITDAYAGKEYIIQVAAK--
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                                    359 GEPSSG 364
                                                                 284 ----DNEIGTWSDWSVAAHATPWTEEPRHLTTEAQAAETTTSTTSSLAPPPTTKICDP--
                                                                                                           320 GIYGSKKAGIWSEWS---
                                                                                                                                                                            261 VSPPALKD-FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPF 319
                                                                                                                                                                                                               168 YMHLFSTIKYKYSISVSNALGH-NATAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTW 226
                                                                                                                                                                                                                                                  203 DLALFT--PYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRW 260
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                                                                                                                                                                                                                                                                                                                                                                                                    92 RILINTSTIALALIANINGSRQQSGDNIVCHARDGSILAGS-CLYVGLPPEKPFNISCWSRN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                        15 AAAAVVYAQRHSPQEAPHVQYERLGSDVTLPCGTANWDAAVT----WRVNGTDLAPD-- 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 18, REFERENCE/DOCKET NUMBER:
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NG DATE: 19910603
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1155 Avenue of the Americas
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26.2%;
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Pred. No. 7.3
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                     321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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                                                                                                                                           Application US/08915495
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RNTION: RECEPTORS FOR HUMAN IL-12
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Hoffmann-La Roche Inc
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300 LY----KGSWSDWSESLRAQTPEEEPTG 323
                                                                                                     261 VSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFG
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Application US/08419652

320 246 197

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INTERLEUKIN-12 RECEPTOR

ffmann-La Roche Inc

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Query Match
Best Local Similarity 31.8
Matches 68; Conservative
175 LCGLLPATAYTLQIRCIRWPL----PGHWSDWS 203
                             301. LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWS 334
                                                                                            121 EAAPPQAGCLQ----LCW--EPWQPGLHINQKCELRHKPQRGEASWALVGPLPLEALQYE 174
                                                                                                                                        243 DVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVE-DSVDWKVVDDVSNQT-SCR 300
                                                                                                                                                                                                                                                                                                                            137 PPEKPFNISC-WSRNMKDLTCRWTPGAHGETFLHTNYSLK-YKLRWYGQ---DNTCEEYH 191
                                                                                                                                                                                                                                  192 TVGPHSCHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVV------TTDPPP 242
                                                                                                                                                                                    61 KDGQSHCCIPRKHLLLYQNMGIWVQAENALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSP 120
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LECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
                                                                                                                                                                                                                                                                                3 PPAIPHNLSCLMNLTTSSLICQWEPGP--ETHLPTSFTLKSFKSRGNCQTQGDSILDCVP 60
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APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy
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PETWARE: Patentin Release #1.0, Version #1.25

RENT APPLICATION DATA:
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31-MAY-1994
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19-JUL-1993
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31.8%; Pred. No. 3.5
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31 of human granulocyte colony-stimulating
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Search completed: September 16, 1999, 20:41:07 Job time: 5436 sec

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Result
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Copyright (c) 1993 - 1998 Compugen Ltd.
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RESULT 2 A36337 A36337 A36337 Imembrane glycoprotein gp130 precursor - human C;Species: Homo sapiens (man) C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998 C;Accession: A36337 R;H1b1 M.; Murakani, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T. Cell 63, 1149-1157, 1990 A;Title: Molecular cloning and expression of an IL-6 signal transducer, gp130. A;Reference number: A36337; MUID:91084844 A;Accession: A36337 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-918 <hib> A;Cross-references: GB:M57230; NID:9186353; PID:9186354 C;Genetics: GB:M57230; NID:9186353; PID:9186354 A;Gene: GDB:IL6ST; GP130</hib>	Ghes 95; Ir ches 95; Ir yellow	ttin receptor long form precursor, hepatocies: Homo sapiens (man) e: 17-Jul-1992 #sequence_revision 17-Jul- ession: A4014 tin, J.M.; Edery, M.; Shirota, M.; Jolico Endocrinol. 3, 1455-1461, 1989 le: Identification of a cDNA encoding a lerence number: A40144; MUID:90114212 ession: A40144 ecule type: mRNA idues: 1-622 CBOUD- ss-references: GB:M31661; NID:g190361; PI etics: e: GDB:PRLR ss-references: GDB:120315; OMIM:176761 position: 5p13 3-5p13.1 position: 5p13 3-5p13.1 position: signal sequence #status predict 622/Product: prolactin receptor, long for 104,233/Binding site: carbohydrate (Asn)	40 188.5 8:1 1162 2 PC4184 41 188.5 8.1 805 3 JC4897 leptin receptor, 0 42 186 8.0 626 2 S37622 proto-oncogene m 43 185 8.0 1092 2 JX0312 differentiation-st 44 185 8.0 719 2 JC2181 differentiation-st 45 182 7.9 895 2 S74225 leptin receptor, i
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A;Map position: 5q11-5q11
C;Keywords: glycoprotein; membrane protein
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A;Title: Prolactin receptor antagonists that inhibit the A;Reference number: A57018; MUID:95286597
A;Accession: A57018
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A; Residues: 1-206 <RES>
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Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
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                                  310 YFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
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                                                                  RKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTEFKILSLHPGQK 177
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YLVQVRCKP--
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Pred. No. 2.4e
25; Mismatches
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A/Experimental source: liver A/Note: sequence extracted fi C/Keywords: transmembrane pro
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A;Reference number: A44257;
A;Accession: A44257
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C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 07-Feb-1997
C;Accession: 149599; 148370
R;Saitc, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
                                                                                                                                                                                                                                                                                                                                                                 R; Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M Genomics 14, 666-672, 1992
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C;Accession: A44257
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C;Keywords: glycoprotein
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Best Local Similarity
Matches 92; Conser
                                                                                                                                               Molecule type: mRNA
Residues: 1-918 <WAN>
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Residues: 1-917 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        339 AST--PRSERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 -- ETYLETNYTLKSE--WATEKFPDCQSKHGT---SCMVSYMPTYYVNIEVWVEAENALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 KVSSESINFDPVDKVKPTPPYNLSVTNSEELSSILKLSWVSSGL--GGLLDLKSDIQYRT
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29.6%;
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; MUID:93052397
                                                                  NCBI
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                                                              backbone
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lactogen receptor 1 - rat
C;Speckes: Rattus norvegicus (Norway rat)
C;Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 10-Sep-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  docrinology 135, 269-276, 1994
Title: Cloning, expression, and mutational analysis
Reference number: I50455; MUID:94283267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               olactin receptor - pigeon
|Species: Columba livia (domestic pigeon)
|Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
|Accession: I50455
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Best Local
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Chen, X.; Horseman, N.D.
1docrinology 135, 269-276, 1994
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Residues: 1-830 <CHE>
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                                                                                                                                                                                                                                                            253
                                                                                                                                                                                  310 YFVQVRCNPFGIYGSKKAGIWSEWS 334
                                                                                                                                                                                                              348 KPYLVLTW-SPPPLADVRSGWLTLDYELRLKPEEAEEWETI-FVGQQTHYKMFSLNPGKK 405
                                                                                                                                                                                                                                                                             288 NSCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLYVDVTYIVQTDPPVNVTLELKKTVNR 347
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                                                                                                                                                          406 YIVQIHCKP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 SGTTYEDRP 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 --ETYLETNYTLKSE--WATEKFPDCRTKH--GTSSCMMGYTPIYFVNIEVWVEAENALG
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                                                                                                                                                                                                                                             EDQLSVRWVSPPALKDF----LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV 309
                                                                                                                                                                                                                                                                                                            HSCHI-PKDLALFTPYEIWVEATNRLGSARSDYLTLDYLDVVTTDPPPDV--HVSRVGGL 252
                                                                                                                                                                                                                                                                                                                                               PPEKPTIIKCRSPEKETFTCWWKPGSDGG---HPTNYTLLYSKEGEERVYECPDYKTAGP 287
                                                                                                                                                                                                                                                                                                                                                                               PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDASTWIQVPLEDTVSPRISFTVQDLKPETEYVFRIR----SIKENGK-GYWSDWSE-EA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVSSEPINFDPVDKVKPSPPHNLSVTNSEELSSILKLAWVNSGL--DSILRLKSDIQYRT
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     E.; Tsai-Morris,
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37.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 314; DB 2;
Pred. No. 1.1e-17;
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1; Mismatches
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Z.Z.;
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C:Species: Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                           Query Match
Best Local S
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                                                                                                                                                                                                                                                                             Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Accession: A36116
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                                                                                                                                                                                                                                                                                                                                                                           Residues: 1-610 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shirota, M.; Banville, D.; Ali, S.; Jolicoeur, C.; Boutin, J.M.; Edery, M.; Djiane, Di. Endocrinol. 4, 1136-1143, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                Title: Expression of two forms of prolactin receptor Reference number: A36116; MUID:91155946
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Best Local 9
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          184
                                                                                                                                                                                                                                 125 SILAGSCLYVGLÞÞERPFNISCWSRNMKDLICRWIPGAHGEIFLHINYSLKYKLRWYGQD 184
                                         297
                                                                           126
                                                                                              242 PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 296
                                                                                                                                                               185 NT--CEEXHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP 241
                                                                                                                                           66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 RNLTL-EVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
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TQFKVFDLYPGQKYLVQTRCKP-----DHGYWSRWSQESSVEMP
                             TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
                                                              RNLTL-EVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ
                                                                                                                                 TIYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP
                                                                                                                                                                                                  SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ
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                                                                                                                                                                                                                                                                             80;
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1-610 <ZHA>
                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                         13.5%;
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Pred. No. 1e-17;
5; Mismatches 85;
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Pred. No. 1e-17;
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RESULT A41070

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                                                                                                                                                                                                                                                                                                   A; Accession: A29884
                                                                                                                                                                                                                                                                                                                                                                                                                                       prolactin receptor precursor -
                                                                                                                                                                                      Keywords: transmembrane protein
1-19/Domain: signal sequence #status predicted <SIG>
20-310/Product: prolactin receptor #status predicted
                                                                                                                                                                                                                                                                                                                 Title: Cloning and expression of the rat
Reference number: A29884; MUID:88165059
                                                                                                                                                                                                                                                                                                                                                                                                   Species: Rattus norvegicus (Norway rat)
Date: 30-Sep-1989 #sequence_revision 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: EMBL:U07567; NID:g641963; Experimental source: Nb2-11C cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: mRNA
                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                         Cross-references: GB:M19304; NID:g206364; PID:g206365
                                                                                                                                                                                                                                                               Molecule type: mRNA
Residues: 1-310 <BOU>
                                                                                                                                                                                                                                                                                                                                                                        Boutin,
                                                                                                                                                                                                                                                                                                                                                                                          Accession:
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                                                                                                          Matches 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 266, 20110-20117, 1991
Title: A prolactin-dependent immune cell line (Nb2) expresses. Reference number: A41070; MUID:92041834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             folecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          )'Neal, K.D.; Yu-Lee, L.Y.
Biol. Chem. 269, 26076-26082, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ross-references:
                                                                 125 SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184
         185
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NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP
                                SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK
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                                                                                                                                                                                                                                                                                                                                                                    J.M.; Jolicoeur, C.; Okamura, H.;
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                                                                                                          Conservative
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92 #sequence_revision
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                                                                                                                            Pred.
                                                                                                                                         Score 312;
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Pred. No.
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on 12-Jun-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DHGYWSRWSQESSVEMP
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                                                                                                                                           DB 2;
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                                                                                                                                       Length 310;
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                                                                                                     Indels 26;
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                                                                            C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision
                                                                                                                                     RESULT
177524
                                                                                                                prolactin receptor precursor - mouse
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Accession:

Davis,

Expression of multiple forms of the sce number: 157699; MUID:89261824

prolactin

receptor

u,

mouse

Linzer, D.I.H. L. 3, 674-680,

02-Aug-1996

#text_change

02-Aug-1996

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A;Residues: 41-58,'x',60-66;90-93,'x',95-96,'x',98-103,'x',105,'NX',108;150-164,'
A;Residues: the amino end of the mature protein was blocked
C;Keywords: blocked amino end; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-616/Product: productin receptor 2 #status predicted <MAT>
F;235-258/Domain: transmembrane #status predicted <MAT>
F;235-258/Domain: transmembrane #status predicted <Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Edery, M.; Jolicoeur, C.; L. Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: prolactin receptor, mammary gland c;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Mar-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Identification and sequence analysis of a second form of prolactin receptor A;Reference number: A30304; MUID:89184578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate
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Matches
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203 LYQVRCKP-----DHGFWSVWSPESSIQIP
                                                                                                                                     256 LSVRWVS--PPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVY 310
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                                                                                                                                                                                                                                                                                                                         137 PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPH 196
                                              311 FVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
                                                                                           144 KPYLWYKWLPPTLYDYRSGWLTLQYEIRLKPEKAAEWE-THFAGQQTQFKILSLYPGQKY 202
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                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                SCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQ 255
                                                                                                                                                                                    SCYFSKKHTSIWTIYIITVNATNQMGSSVSDPRYVDVTYIVEPDPPVNLTL-EVKHPEDR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                 PPGKPFIFKCRSPEKETFTCWWRPGADGG--LPTNYTLTYHKEGETITHECPDYKTGGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TQFKVFDLYPGQKYLVQTRCKP-----DHGYWSRWSQESSVEMP
                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          13.3%;
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                                                                                                                                                                                                                                                                                                                                                                                    28,
                                                                                                                                                                                                                                                                                                                                                                               Score 307.5;
Pred. No. 2.4e
28; Mismatches
                                                 342
                                                                                                                                                                                                                                                                                                                                                                                                          2.4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 616;
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A; Accession:

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prolactin receptor precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: 177525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Davis, J.A.; Linzer, D.I.H.
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                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: mRNA
Residues: 1-292 <RES>
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Best Local Similarity
Matches 85; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: mRNA; Residues: 1-303 <RES>
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   206
                                 322
                                                    150 TITDVKTGWFTMEYEIRLKSEEADEWE-IHFTGHQTQFKVFDLYPGQKYLVQTRCKP---
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                                                                                                                                                                  207
                                                                                                                                                                                                       150 NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNT--CEEYHTVGPHSCHIPKD-LAL 206
                                                                                                                                  91
                                                                                                                                                                                 35 DKETFTCWWNPGSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 ALKDF---LFQAKYQIRYRVEDSYDWKYYDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 FTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVS--PP 264
                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNT--CEEYHTVGPHSCHIPKD-LAL 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 LSRLLNTSTLALALANLNGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSR 149
                                                                                   ALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 321
                                                                                                                    WKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP
                                                                                                                                                   FTPYEIWVEATURLGSARSDYLTLDYLDVYTTDPPPDVHVSRVGGLEDQLSVRWVS--PP 264
                                                                                                                                                                                                                                                                                LSRLINTSTLALALANINGSRQQSGDNLVCHARDGSTLAGSCLYVGLPPEKPFNISCWSR 149
                            YGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                          MSSALAYMLLVLSISLLNG---QS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WKIYIITVNATNEMGSSTSDDLYVDVTYIVEDEDPRNLTL-EVKQLKDKKTYLWVKWLPP 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                          13.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1989
                                                                                                                                                                                                                                                                                                                           37;
                                                                                                                                                                                                                                                                                                                      ; Score 307.5; I
; Pred. No. 9.2e
37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forms of the prolactin
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Pred. No. 9.6e-18;
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les 92;
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RESULT
                                                                        prolactin receptor precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
C;Accession: JQ1655
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            Ochem. Biophys. Res. Commun. 188, 'Title: Double antenna structure of
                                                         Tanaka, M.;
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Best Local S
Matches 85
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A;Title: Changes in prolactin receptor expression during pregnancy
A;Reference number: I53269; MUID:93307149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comment: Prolactin receptor have long form and short form which are resulted from a (Comment: This long form receptor is capable of transducing a signal to milk protein (Reywords: receptor) transmembrane protein (230-253/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Molecule type: mRNA;Residues: 1-557, F',559-608 <EDE>;Residues: 1-557, F',559-608 <EDE>;Residues: 1-557, F',559-608 <EDE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: S34356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reference number: S34356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description: Isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross references: GB:L13593; NID:g347398; PID:g347842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: mRNA Residues: 1-608 < MOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title: Cloning and sequencing of the cDNA encoding Reference number: JT0671; MUID:94085788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Edery, M.; Pezet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:L14811; NID:g293769; PID:g293770 Moore, R.C.; Oka, T.
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Accession: I53269; JT0671; S34356
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                                                                                                                                                                                                                                                                        322 YGSKKAGIWSEWSHPTAASTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                   ----DHGYWSRWGQEKSIEIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary; translated from GB/EMBL/DDBJ
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                                               Maeda, K.; Okubo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Oka, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                               T.; Nakashima, K.
                                                                                                                                                                                                                                                                        342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 307.5; DB 2;
Pred. No. 2.4e-17;
7; Mismatches 92;
                               490-496,
      chicken
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      prolactin
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      deduced
                                                                                10-Sep-1997
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the cDNA
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A;Molecule type: mrNA
A;Residues: 1-831-CTANA
A;Cross-references: DDBJ:D13154; NID:g222848; PID:d1002939; PID:g222849
A;Cross-references: DDBJ:D13154; NID:g222848; PID:d1002939; PID:g222849
A;Experimental source: kidney
C;Keywords: glycoprotein; transmembrane protein
F;1-37/Domain: signal sequence #status predicted <SIG>F;24-831/Froduct; prolactin receptor #status predicted <ART>
F;439-682/Domain: transmembrane #status
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Search completed: September 16, 1999, 20:42:07 Job time: 5400 sec

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GenCore version 4.5 Compugen Ltd.
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:un on: M protein protein search, using sw model September 17, 1999, 03:10:12; Search time 35.09 Seconds (without alignments) 342.377 Million cell updates/sec

erfect score: itle: equence: US-09-037-657-15 2317 MPAGRPGPVAQSARRPPRPL..........NQDEGILPSGRRGAARGPAG 425

earched: 77977 seqs, 28268293 residues coring table:

BLOSUM62

atabase : SwissProt_37:*

Pred. No. score grea and is der No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

mus musculu	*							
2	מלא מלא		GHRL MOUSE	_	297	6.1		43
5	01693		GHRH MOUSE	_	650	6.1		42
++115	P16310				638	٠	143	÷ ÷
mo sapi	Q14627	•	I 132_HUMAN		380	•	٠.	
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-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The X-ray structure of a growth hormone-prolactin receptor NATURE 372:478-481(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOUTIN J.-M., EDERY M., SHIROTA M., JOLICOEUR C., LESUEUR L., ALI S., GOULD D., DJIANE J., KELLY P.A.; "Identification of a cDNA encoding a long form of prolactin receptor in human hepatoma and breast cancer cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS (HUMAN).
FUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                  FAM; PF000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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15, LAST SEQUENCE UPDATE)
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                                                                                        69505 MW;
               14.38;
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                                                                                                                                                                                                                                                                                                    GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.
 Score 331; DB
Pred. No. 1.8e
27; Mismatches
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POTENTIAL.
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BY SIMILARITY.
                                                                                                                                                                                     FIBRONECTIN TYPE-III.
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                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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EMBL; M57230;
PIR; A36337; A
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P40189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     )1-FEB-1995 (REL. 31, CREATED)
11-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIMATES;
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ONE IG-LIKE DOMAIN.

SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

DATABASE: NAME-PROW; NOTE-CD guide CD130 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd130.htm".
                                                                                                                                                                                                                                                               FUNCTION: SIGNAL TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR LIL-5, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIAT. SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLIRESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITE: AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLL BENERYONIC DEVELOPMENT (BY SIMILARITY).

SUBGUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

SUBGULILAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS.
                                                                                                                                                                                                                                                     SIMILARITY:
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RYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                          17:1665-1674(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                     , STAUNTON D., HEATH J.K., JONES E.Y.; structure of a cytokine-binding region of gp130.";
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n IL-6 signal
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA)
INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA)
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                                                                                                                                             STPRSERP 347
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                                                                                                                                                              DASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIRC
                                                                                                                                                                               DSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAA 339
                                                                                                                                                                                                    VTSDHINFDPYKVKPNPPHNLSVINSEELSSILKLTWTN-PSIKSVII-LKYNIQYRTK
                                                                                                                                                                                                                                        --ETHLETNETLKSEWATHKFADCKAKRDT--PTSCTVDYSTVYFVNIEVWVEAENALGK 206
                                                                                                                                                                                                                                                                                                                     ISPESPVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVT
                                                                                                                                                                                                                                                                                                                                                             88;
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                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-98.
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           43
131
157
227
379
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124
325
518
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                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                     14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                           Score 329; DE
Pred. No. 4.26
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIBRONECTIN
FIBRONECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIBRONECTIN
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                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERLEUKIN-6
                                                                                                                                                                                                                                                                                                                                                                                                          7CC06F05 CRC32;
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                                                                                                                                                              ----MKEDGKGYWSDWSEEASG
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                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                               918;
                          (INTERLEUKIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART,

SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES
EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA;
RODENTIA; S
                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MBL; X62646; G840817; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning of a murine II-6 receptor-associated signal transducer, gp130, and its regulated expression in vivo.";
J. IMMUNOL. 148:4066-4071(1992).
                                                                                                                                                                                                                ARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES DURING THE REST OF EMBRYOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INTITATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ONE IG-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:96560; IL6ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00340; RECEPTOR_CYTOKINES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-MACROPHAGE
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                                                           61
83
131
157
225
476
          102452 MW;
POTENTIAL.
/; A5DCD259 CRC32;
                                                                           POTENTIAL.
POTENTIAL.
                                                      POTENTIAL
                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                           TYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERLEUKIN-6 RECEPTOR BETA CHAIN
                                                                                                                                                                                                                                                                                                                                  BRONECTIN TYPE-III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOT RESTRICTED TO IL-6-RESPONSIVE
                                                                                                                                                                                                                                                         SIMILARITY.
                                                                                                                                                                                                                                                                                 SIMILARITY.
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LINES TESTED
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Query Match

13.8%;

Score 319.5;

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Length 917;

EMBL; M92340;

NOT_ANNOTATED_CDS

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RESULT
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             the European Bioinformatics institute. There as a use by non-profit institutions as long as a modified and this statement is not removed. Use entitles requires a license agreement (See http
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL6B_RAT P40190;
or send an email to license@isb-sib.ch)
                                                                                                                  This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and charact transducing molecule, gp130."; GENOMICS 14:666-672(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WANG Y., NESBITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATTUS NORVEGICUS (RAT). EUKARYOTA; METAZOA; CHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RODENTIA; SCIUROGNATHI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERLEUKIN-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 GTTYEDRPSRP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 AST--PRSERP 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 KDASTWIQVPLEDIMSPRISFIVQDLKPFTEYVFRIR----SIKDSGK-GYWSDWSEEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 KVSSESINFDPVDKVKPTPPYNLSVTNSEELSSILKLSWVSSGL--GGLLDLKSDIQYRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 --ETYLETNYTLKSE--WATEKFPDCQSKHGT---SCMVSYMPTYYVNIEVWVEAENALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 SARSDYLTLDYLDYYTTDPPDDYHYSRYGGLEDQLSYRWYSPPALKDFLFQAKYQIRYRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 HGETFLHTNYSLKYKLRWYGQD-NTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 LANLNGSRQQSGDNLYCHARDGSILAGSCLYYGLPPEKPFNISCWSRNMKDLTCRWTPGA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 FTDVVLPSVQLTCNILSFGQIEQNVTGVTMLSGFPPDKPTNLTCIVNEGKNMLCQWDPGR 150
                                                                                                                                                                                                                                                                                                                                                 FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP110 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6/E (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
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                                                                                                                                                            SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                               AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE EMERYONIC DEVELOPMENT (BY SIMILARITY).
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FI
                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. ONE IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                      AND ENDOTHELIAL CELLS.
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IHI; MURIDAE; MURINAE; RATTUS.
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0; Mismatches 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FULLER G.M.; on of the rat liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        918 AA
           (See http://www.isb-sib.ch/announce/
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Best Local Similarity 29.8%;
Matches 92; Conservative
                                             Q90374;
01-NOV-1997
01-NOV-1997
15-JUL-1998
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DOMAIN
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RECEPTOR; TRANSMENT
PRLR.
COLUMBA LIVIA (DOMESTIC PIGEON).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
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                                                                                              PRLR_COLLI
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                                                                                                                                                                                                                                                                                                                                                                                      103
                                                                                                                                                                                                                                                                                                                                                        91 FTDVVFQNVQLTCNILSFGQIEQNVYGITILSGYPPDIPTNLSCIVNEGKNMLCQLDPGR
                                                                                                                                                                                                                                                                                                                                                                                                            31
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                                                                                                                                                                                                                      EDSYDWKYV---DDYSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTA
                                                                                                                                                                                                                                                       NVSSEPINFDPVDKVKPSPPHNLSVTNSEELSSILKLAWVNSGL--DSILRLKSDIQYRT
                                                                                                                                                                                                                                                                              SARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRV
                                                                                                                                                                                                                                                                                                       --ETYLETNYTLKSE--WATEKFPDCRTKH--GTSSCMMGYTPIYFVNIEVWVEAENALG
                                                                                                                                                                                                                                                                                                                               HGETFLHTNYSLKYKLRWYGQD-NTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLG
                                                                                                                                                                                                                                                                                                                                                                                                                               ISPODPTLLIGSSLOATCSIHG---DTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A44257;
                                                                                                                                                          SCITYEDRP
                                                                                                                                                                                  ASTPRSERP 347
                                                                                                                                                                                                                                                                                                                                                                                LANLINGSROQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGA 162
                                                                                                                                                                                                                                                                                                                                                                                                         IYPEFPVVQRGSNFTATCVLKEKCLQVYSVNATYIVWKTNHVAVPKEQVTVINRTASSVT
                                                                                                                                                                                                         KDASTWIQVPLEDTVSPRTSFTVQDLKPFTEYVFRIR----SIKENGK-GYWSDWSE-EA
                                  RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEMBRANE;
                              (REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UI
(REL. 36, LAST ANNOTATION
ECEPTOR PRECURSOR (PRL-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A44257
                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR_CYTOKINES_2;
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                                           LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 317.5; DB 1;
pred. No. 3.7e-18;
51; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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FIBRONECTIN TYPE-III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERLEUKIN-6
                                                                                              PRT;
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                                                                                              830
                                             UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 918;
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PROSITE; PS00241; RECEPTOR_CYTOKINES_1;
PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00041;
HSSP; P16471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. between the Swiss Institute of Biol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA;
NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 94283267.
CHEN X., HORSEMAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                              196
                                                                                    231
                                                                                                        137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
   348
                                                      HSCHI-PKDLALFTPYEIWVEATNRLGSARSDYLTLDVLDVVTTDPPPDV--HVSRVGGL
                                                                                PPEKPTIIKCRSPEKETTTCWWKPGSDGG---HPTNYTLLYSKEGEERVYECPDYKTAGP
                                        NSCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLYVDVTYIVQTDPPVNVTLELKKTVNR
                                                                                                    PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP 195
KPYLVLTW-SPPPLADVRSGWLTLDYELRLKPEEAEEWETI-FVGQQTHYKMFSLNPGKK
                     EDQLSVRWVSPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV
                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAZOA; CHORDATA; VERTEBRATA; ARCHOŞAURIA; AVES; COLUMBIFORMES; COLUMBIDAE; COLUMBA.
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POTENTIAL
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                                                                                                                           29;
                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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                                                                                                                                                                             POTENTIAL.
POTENTIAL.
1; SEFADD51
                                                                                                                                    Score 314; DB 1;
Pred. No. 6.2e-18;
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                                                                                                                          Mismatches
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                                                                                                                                                                             CRC32;
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There are no rest
ng as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prolactin
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                                                                                                                          Gaps
 405
                     309
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                Differential signal transduction of the short, rolactin receptors. Activation of interferon receptors. Activation of interferon result proliferation.";
1. BIOL. CHEM. 269:26076-26082/10041
                                                                                                                                                                                                                                                                                                                                     - FUNCTION: THIS IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHIROTA M., BANVILLE D., ALI S., JOLICOEUR C., BOUTIN J.M., EDERY M., DJIANE J., KELLY P.A.; "Expression of two forms of prolactin receptor in rat ovary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIR_RAT STANDARD; PRT; 610 AA P05710; Q63451; Q63723; Q62832; Q64274; Q63 01-NOV-1998 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A. (FORM NB2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RATTUS NORVEGICUS (RAT)
EUKARYOTA; METAZOA; CHOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEAL K.D., YU-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A. (FORM NB2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OUTIN J.-M., JOLICOEUR C., OKAMURA H., GAGNON J., EDERY M., HIROTA M., BANVILLE D., DUSANTER-FOURT I., DJIANE J., KELLY P.A.; Cloning and expression of the rat prolactin receptor, a member of the growth hormone/prolactin receptor gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ODENTIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eceptor cDNA species."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HANG R., BUCZKO E., TSAI-MORRIS C.H., ISOlation and Characterization of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSUE-LYMPHOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QUENCE OF 281-610 FROM N.A.

INVILLE D., STOCCO R., MURTHY K.K., BOIE Y., KELLY P.A.;
BMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JBMITTED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I S., PELLIGRINI I., KELLY P.A.; prolactin-dependent immune cell line prolactin receptor.";
                                                                                                                                                                           SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED BY AL
SPLICING OF THE PRLR GENE.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         YU-LEE L.Y.;
                                                                                                                                                                                                                                                                                                                      269:26076-26082(1994).
HIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
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EY; TISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMUN. 168:415-422(1990).
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Q62832; Q64274; Q63479;
                   (See http:/
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(LACTOGEN RECEPTOR).
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Best Local s
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  PRIR_MOUSE STANDARD;
Q08501; Q62099; P15213; P1
01-APR-1990 (REL. 14, CREA
01-FEB-1995 (REL. 31, LAS]
15-JUL-1998 (REL. 36, LAS]
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                                                                                                                                                                                                              185 NT -- CEEYHTVGPHSCHIPKD-LALFTPYEIWVEAINRLGSARSDVLILDVLDVVTIDPP 241
                                                                                                                                                                                                                                                           125 SILAGSCLYYGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                          66 TTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP
                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                    Local
                                                                                                 TQFKVFDLYPGQKYLVQTRCKP-----DHGYWSRWSQESSVEMP 222
                                                                                                                       TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                             RNLTL-EVKQLKDKKTYLMVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ
                                                                                                                                                                                                                                     SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                                                                                                                                                                                                                                                                           80
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                                                                                                                                                                                                                                                                                                    Similarity
(REL. 14, CREATED)
(REL. 31, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPLICING.
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68599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.

EVKOKKNKTYLMYKWSPPT -> DYRWEVSCH
KLM (IN SHORT FORM).

MISSING (IN SHORT FORM).

KGKSEELLSALGCQDFPPTSDCEDLLVEFL -:

TGSPSKYKVDLYLALPGGFQKLDNAGELDY (:
                                                                                                                                                                                                                                                                                                Score 312; DB 1;
Pred. No. 6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM FORM)
MISSING (IN
MISSING (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (BY SIMILARITY).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROLACTIN RECEPTOR.
EXTRACELLULAR (BY SIMILARITY).
BY SIMILARITY.
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BY SIMILARITY.
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(IN REF. 2).
(IN REF. 1).
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TTTTE REGION OF THE REGION OF 
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EMBL; D10214;
EMBL; X73372;
EMBL; M22959;
                                                                                                                                                                                                                                                 PIR; JT06
MGD; MGI:
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
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STRAIN-SWISS WEBSTER; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L13593; G347842; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 89261824.
DAVIS J.A., LINZER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 9408578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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EUKARYOTA; METAZOA; CHOI
RODENTIA; SCIUROGNATHI;
  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SWISS WEBSTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDERY M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENDOCRINOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'cloning and sequencing of the long-form prolactin receptor."; ENE 134:263-265(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROLACTIN RECEPTOR PRECURSOR (PRL-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Changes in prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression of multiple forms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LARKE D.L., LINZER D.I.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENE.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PONCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY PROLACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALTERNATIVE PRODUCTS: THREE FORMS, PRL-R1, PRL-R2 AND PR (SHOWN HERE) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                    PS00241; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , PEZET A., N
D (JUN-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JUL-1992)
                                                                                                                                      TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M N.A. (FORM PRL-R3).
TISSUE-MAMMARY GLAND;
  20 230
                                                                                                             SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINZER D.I.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-MAMMARY GLAND;
T A., NANDI S., KELLY P.A.;
-1993) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3:674-680(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FORM
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THI: MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            institutions as long as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TO EMBL/GENBANK/DDBJ DATA BANKS.
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                                                                                                                                 GLYCOPROTEIN;
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PROLACTIN RECEPTOR. EXTRACELLULAR (BY S BY SIMILARITY.
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KELLY P.A.;
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                                                                                                                                      SIGNAL; REPEAT;
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                                                                                                                                                                                                                       FALSE_NEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the murine mammary gland
                            SIMILARITY).
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Matches
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                                                                                                                                                                                                                                                                                                                     PRLR_RABIT P14787;
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                EDERY M., JOLICOEUR C., LEVI-MEYRUEIS PETRIDOU B., BOUTIN J.M., LESUEUR L., "Identification and sequence analysis receptor by molecular cloning of compl mammary gland.";
PROC. NATL. ACAD. SCI. U.S.A. 86:2112-
                     receptor.";
PROTEINS 27:459-468(1997
                                                                                                                                                                                                                                    ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                     01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
15-70L-1998 (REL. 36, LAST ANNOTATION UPDAT
PROLACTIN RECEPTOR PRECURSOR (PRL-R).
                                                                                                                                                                                                                                                                                                                                               RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                 3D-STRUCTURE MODELLING MEDLINE; 97248733.
                                                     HALABY D., THOREAU
                                                                                                                                                                      TISSUE-MAMMARY GLAND;
MEDLINE; 89184578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150
                                                                                                                                                                                                                                                                                                                                                                                            206
                                                                                                                                                                                                                                                                                                                                                                                                                                          150
                                           Homology modeling
                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                        AGOMORPHA; LEPORIDAE;
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        FUNCTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKETFTCWWNPGSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI
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                                                                                                                                                                                                                                                                                                                                                                                                                    YGSKKAGIWSEWSHPTAASTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP
                                                                                                                                                                                                                                                                                                                                                                                            ----DHGYWSRWGQEKSIEIP
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        THIS IS A RECEPTOR
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                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                           o H
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                                           rabbit
                                                       DJIANE
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                                                                                                                                                                                                                          ORYCTOLAGUS
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                                                                              30-228
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L -> F (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 307.5;
Pred. No. 1.
                                          prolactin hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.

KGKSEELLSALG -> VHNKEQLENYVY (IN PRL-R2).

MISSING (IN PRL-R2).

KGKSEELLSALGCQDFPPTSDCE -> LWCSILQLTSLVKI

PTTEFLCDL (IN PRL-R1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (BY SIMILARITY).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                     86:2112-2116(1989)
                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSING (IN PRL-R1).
-> F (IN REF. 2).
AA401E67 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
         FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                             complementary
                                                                                                                                                                                                                                                                                                                                  616
                                                                                                                                       C., DUSANTER-FOURT
KELLY P.A., DJIANE
of a second form o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.4e-17;
ches 92;
                                                                                                                                                                                                                                     MAMMALIA;
                                                                                                                             DNA
                                           complexed
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                                                                                                                                                                                                                                     EUTHERIA;
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f
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                                            with
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                 01-JUN-1994
01-JUN-1994
15-JUL-1998
                                                                                                                                                                                                                                                        PRLR_CHICK
Q04594;
                                                                                                                                                                                                                                                                                               CHICK
                                        STRAIN-WHITE LEGHORN; TISSUE-KIDNEY;
MEDLINE; 93075121.
                                                                         SEQUENCE FROM N.A.
                       TANAKA M.,
                                                                                                                                 EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A30304;
PDB; 1AN3; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                   311
                                                                                                                                                                                                                                                                                                                                                                                                                            144 KPYLWVKWLPPTLVDVRSGWLTLQYEIRLKPEKAAEWE-THFAGQQTQFKILSLYPGQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J04510; G165670;
                                                                                                                                                                         1-JUN-1994 (REL. 29, CREATED)
1-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
5-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
ROLACTIN RECEPTOR PRECURSOR (PRL-R) (CPRLP).
                                                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 PPEKPENISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPH 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARBOHYD
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                                                                                                              EOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
mes 77; Conserv
                                                                                            LUS GALLUS (CHICKEN).
ARRYOTA; METAROA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                            LVQVRCKP-----DHGFWSVWSPESSIQIP
                                                                                                                                                                                                                                                                                                                                                                                           FVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCYFSKKHTSIWTIYIITVNATNQMGSSVSDPRYVDVTYIVEPDPPVNLTL-EVKHPEDR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHI-PKDLALFTPYEIWVEATNRLGSARSDYLTLDVLDVVTTDPPPDVHVSRVGGLEDQ 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPGKPFIFKCRSPEKETFTCWWRPGADGG--LPTNYTLTYHKEGETITHECPDYKTGGPN 84
     antenna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00241; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2;
MAEDA K., OKUBO T., NAKASI
tenna structure of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 307.5; DB 1; Pred. No. 1.4e-17;
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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                       PRT;
NAKASHIMA K.;
hicken prolactin receptor deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FB6170B1 CRC32;
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                                                                                                                                                                                                                                                                     831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL; REPEAT; 3D-STRUCTURE.
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PRLR_MELGA RESULT

PRIR_MEIGA STÂNDARD; PRT; 831 AA Q91094; Q91091; Q91092; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

831 AA

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CARBOHYD
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405 YIIQIHCKP-----DHHGSWSEWSSENYIQIPNDFR 435
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                   310 YFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSER 346
                                                                      347 KPYLVLTW-SPPPLADVRSGWLTLEYELRLKPEEGEEWETI-FVGQQTQYKMFSLNPGKK 404
                                                                                                                                        287 NSCYFDKKHTSFWTIYNITVRATNEMGSNSSDPHYVDVTYIVQPDPPVNVTLELKKPINR 346
                                                                                                                                                                           196 HSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDV--HVSRVGGL
                                                                                                                                                                                                                230 PPEKPTIIKCRSPEKETFTCWWKPGLDGG---HPINYTLLYSKEGEEQVYECPDYRTAGP
                                                                                                                                                                                                                                                 137 PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMAIN
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the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the cDNA sequence.";
BIOCHEM. BIOPHYS. RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PS00241; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                           Local Similarity les 76; Conserv
                                                                                                   EDQLSVRWVŠPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV 309
                                                                                                                                                                                                                                                                                                                                                                                    831 AA;
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                    94102
                                                                                                                                                                                                                                                                                                        13.2%; Score 306; DB 1; 35.0%; Pred. No. 2.8e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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                                                                                                                                                                                                                                                                                         96;
                                                                                                                                                                                                                                                                                                                       Length 831;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entitles requires a license agreement (See
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                                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MELEAGRIS GALLOPAVO (COMMON TURKEY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA;
NEOGNATHAB; GALLIFORMES; MELEAGRIDIDAE; MELEAGRIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00340; RECEPTOR_CYTOKINES_1;
PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZHOU J.F., ZADWORNY D.,
SUBMITTED (JUN-1996) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998
PROLACTIN RI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAIN
                                        196
                                                                          230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
NSCYFDKKHTSFWTVYNITVKATNEMGSNSSDPHYVDVTYIVQPDPPANVTLELKKPINR 346
                                                                                                      PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP
                                  HSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDV--HVSRVGGL 252
                                                                   PPEKPTITKCRSPEKETFTCWWKPGLDGG---HPTNYTLLYSKEGEEQVYECPDYRTAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U22947; G973165; -
U22924; G973166; -
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                                                                                                                                        Similarity 35.977; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 email to license@isb-sib.ch).
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                                                                                                                                                                                                                                  A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36, LAST ANNOTATION UPDATE)
R PRECURSOR (PRL-R) (TPRLR).
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TO EMBL/GENBANK/DDBJ DATA BANKS.
A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GUEMENE D., KUNHLEIN U.; EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                  Ę
                                                                                                                                            25;
                                                                                                                                                           Score 305; ;
                                                                                                                                       Pred. No. 3.3e
5; Mismatches
                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENT FIBRONECTIN TYPE-II
                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROLACTIN RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                              FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
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                                                                                                                                                           DB 1;
.3e-17;
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   Query Match
Best Local S
Matches 76
                                                           CARBOHYD
CARBOHYD
SEQUENCE
                                                                                               DOMAIN
DISULFID
DISULFID
CARBOHYD
                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                       PROSITE;
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use by non-profit institutions as lone
modified and this statement is not remove
entitles requires a license agreement (So
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Expression of the prolactin receptor gene during the breedi non-breeding seasons in red deer (Cervus elaphus): evidence expression of two forms in the testis.";
J. ENDOCRINOL. 146:313-321(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-UUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CERVUS ELAPHUS (RED DEER).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                EMBL; X94953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLARKE L.A., EDERY M.,
KELLY P.A., JABBOUR H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q28235
                                                                                                                                                                      FRANSMEN
                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                ISSP; P14787
                                                                                                                                                                                                                                               FAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 96030711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CERVUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARTIODACTYLA;
                                                                                                                                                                                                                                                                                                                                                                                                 1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405 YIVOIHCKP-----DHHGSWSEWSSENYIEIPNDFR 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSER 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPYLMLTW-SPPPLADVRSGWLTLDYELRLKPEEGEEWETV-FVGQQTQYKMFSLNPGKK 404
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              Similarity
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                                                                                                                                                                                                                    TRANSMEMBRANE;
                                                             581 AA;
                                                                                                                                                                                                                                                                               E218406;
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                                                                                    227
46
86
59
132
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              13.1%;
                                                              65159
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                                                                                                                                                                                                                   GLYCOPROTEIN;
                                                             Œ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATA; VERTEBRATA; MAMMALIA; EUTHERIA; PECORA; CERVOIDEA; CERVIDAE; CERVIN
36; Mismatches 92
                                                                                                                                                                                                                                                                                                                              is not removed
                                                          POTENTIAL.
721F0366 CRC32;
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                                                                                                         BY SIMILARITY.
BY SIMILARITY.
                                                                                    POTENTIAL.
                                                                                                                                                FIBRONECTIN
                                                                                               POTENTIAL.
                                                                                                                                 FIBRONECTIN TYPE-III
                                                                                                                                                                     POTENTIAL
                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                             RECEPTOR
                                                                                                                                                                                                                   SIGNAL; REPEAT.
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                                                                                                                                               (POTENTIAL).
TYPE-III.
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                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PITUITARY HORMONE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POSTEL-VINAY M.C.
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     Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; I
                                                                                                                                                                                                        MAIN
                                                                                                                                                                                                                        OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  MBL; L02549; G163618; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial antities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to licenseelsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    ROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997
01-NOV-1997
15-JUL-1998
                                                                                                                                                            ISULFID
                                                                                                                                                                                                                                                                                                                           ECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MODIT P., KESSLER M.A., SCHULER L.A.;
Molecular cloning of the bovine prolactin receptor and prolactin and growth hormone receptor transcripts in tero-placental tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDLINE; 93246019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROLACTIN RECEPTOR PRECURSOR (PRL-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLR_BOVIN
28172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISSUE=ENDOMETRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THIS IS A RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANLTL-ELKHPEDRKPYLWIKWFPPTLTDVKSGWFMIQYEIRLKPETAADWE-IHFAAKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENDOCRINOL. 89:47-58(1992).

ON: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                     581 AA;
         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
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                     13.1%;
                                                                                                   65153
                                                                                                   MW;
       38;
   Score 302.5; DB 1;
Pred. No. 3.4e-17;
38; Mismatches 92;
                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                            FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                         POTENTIAL
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                                       Length 581;
 Indels
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; BOVINAE;
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 47;
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Gaps
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        CARBOHYD
CARBOHYD
                                               DISULFID
                                                                                           DOMAIN
                                                                                                              DOMAIN
                                                                                                                                    DOMAIN
                                                                                                                                                     TRANSMEM
                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                          PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                           EMBL; L34783; G903847; -
                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SANDRA O., SOHM F., DE LUZE A., PRUNET P., EDERY M., KELLY P.A.; "Expression cloning of a cDNA encoding a fish prolactin receptor PROC. NATL. ACAD. SCI. U.S.A. 92:6037-6041(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OREOCHROMIS NILOTICUS (NILE TILAPIA) (TILAPIA NILOTICA).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA; PERCIFORMES;
LABROIDEI; CICHLIDAE; TILAPIA.
                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDLINE; 95320210.
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)1-NOV-1997 (REL.
5-JUL-1998 (REL.
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Q99062;
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                                                          "Functional domains receptor.";
                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 92091782.
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LARSEN A., DAVIS T., CURTIS
PARK L., SORENSEN E., MARCH
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HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                EMBO J. 10:2855-2865(1991).
                                                                                                                                                                                 "Three different mRNAs factor receptor.";
                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR
                                                                             TUKUNAGA R.,
                                                                                                                                                                                                              FUKUNAGA R., SETO Y.,
                               STRUCTURE BY NMR OF 227-334.
                                                                                                                                                                                                                      MEDLINE; 91062348.
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          AMASAKI K., NAITO S., ANAGUCHI H.,
                                                                                              OMAINS STRUCTURE.
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                     97331327
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148:259-266(1992).
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containing the WSxWS
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NAT. STRUCT. BIOL.
                                         motif of the granulocyte colony-stimulating interaction with ligand.";
3D-STRUCTURE MODELLING OF 125-331.
                             4:498-503(1997).
                                                              factor receptor
                                                          and
                                                              its
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LAYTON J.E., IARIA J., SMITH D.K., TREUTLEIN H.R.;
"Identification of a ligand-binding site on the granulocyte
stimulating factor receptor by molecular modeling and mutage
J. BIOL. CHEM. 272:29735-29741(1997).
-I- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FAranulocyte colony-and mutagenesis.";

CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR EVENTS AT THE CELL SURFACE. FACTOR (G-RECOGNITION

SUBUNIT: DIMER (PROBABLE)

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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM, WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM

OF THE RECEPTOR.

OF THE RECEPTOR.

OF THE RECEPTOR.

INSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN BONE MARROW CELLS, PLACEWYA, AND PERIPHERAL BLOOD GRANULOCYTES.

THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE GCSER-3 FORM IS HIGHLY EXPRESSED TO THACENTA.

ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS, GCSFR-1 (SHOWN UNDER), GCSFR-2, GCSFR-3 AND GCSFR-4/D7, ARE PROBABLY PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY DIFFER IN THEIR C-

TERMINAL PORTION.

ALSO KNOWN AS SEVERE SIMILARITY: BELONGS 1 SIMILARITY: BELONGS TO ONE IG-LIKE DOMAIN. TS IN CSF3R ARE A CAUSE OF KOSTMANN SYNDROME; SEVERE CONGENITAL NEUTROPENIA (SCN).
LONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. DATABASE: NAME-PROW; NOTE-CD guide CD114 entry; www.ncbi.nlm.nih.gov/prow/cd/cd114.htm".

the European Bioinformatics Institute. The second of the statement is not removed entities requires a license agreement (Second entities requires a license agreement (Second entities requires a license agreement (Second entities requires a license@isb-sib.ch). SWISS-PROT entry is copyright. It is produced through a cen the Swiss Institute of Bioinformatics and the EMBL is not removed (See http://www.isb-sib There are no restrictions as its content and collaboration -L outstation outstation ö ဝ္

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RECEPTOR_CYTOKINES_2; SPLICING; FIBRONECTIN FIBRONECTIN BY SIMILARIT IG-LIKE C2-TYPE DOMAIN FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III. CYTOPLASMIC (POTENTIAL) GRANULOCYTE COLONY EXTRACELLULAR (POTENTIAL)
POTENTIAL. RECEPTOR 3D-STRUCTURE. SIMILARITY TYPE-III <u>- -</u> STIMULATING FACTOR SIGNAL;

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01-FEB-1995 (REL. 3:
15-JUL-1998 (REL. 3:
GRANULOCYTE COLONY :
SEQUENCE FROM N.A. MEDLINE; 90235283.
                           MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
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                                                                                                                              GCSR_MOUSE
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                                                                                                                                                                                                                                           PPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVE-DSVDWKVVDDVSNQT-S
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                                                                                                                                                                                                                                                                               YHTVGPHSCHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVV------TTDP
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                                                               OR CSFGR
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97; Conser
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                                                                     (REL: 31, CREATED)
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CCLONY STIMULATING FACTOR RECEPTOR
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Pred. No. 4.
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ANAT: STRUCT. BIOL. 4:498-504(1997).

-1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR. IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVENTS
THE CELL SURFACE:
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FIBRONECTIN TYPE-III.
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                          01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.NOV-1998 (TrEMBLrel. 08, Last annotation update)
PROLACTIN RECEPTOR (FRAGMENT).
                                                               Q16354;
01-NOV-1996
   Eukaryota;
               Homo sapiens (Human)
                                                                                           Q16354
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Ekkaryota; Metazoa; Chordata; Craniata; Ver
Batrachia; Anura; Mesobatrachia; Pipoidea;
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SHEN J., GRACE A., CHIEN K.R.;
SUBMITTED (JAN-1998) to the EMBL/GenBank/DDBJ
EMBL; AF041845; AAC03531.1; -
FFAM; PF00041; fn3; 4.
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1-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                          50 DPTLLIGS-SIQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        SROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFL 168
                                                                                                                                                                                                                        VEDSVDWKVV----DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPT
                                                                                                                                                                                                                                               GIQKSETLTIDPVNIVKPNPPQLSELISSLELPNALKIEWKNPIT---NAFNLKYNIRYR
                                                                                                                                                                                                                                                                 GSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYR
                                                                                                                                                                                                                                                                                                 PTNYTLSH--RWAHFGANYCRGANNSC-----TIHSP-GFQFYIDTTFQVEATNEL
                                                                                                                                                                                                                                                                                                                       HTNYSLKYKLRW------YGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRL
                                                                                                                                                       KQVTP - - EAP -
                                                                                                                                                                           AASTPRSERPGPGGGVCEPRGGEPSSGP
                                                                                                                                                                                                                                                                                                                                                 LNSPLTCNVMASGHVANTLYGIFFTLGLPPDKPTNLTCIVYNQDNLTCTWDPGR--PTNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWWQKSHKTRNQDEGILPSGRRGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         100;
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     Metazoa;
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8 (TrEMBLrel.
9 (TrEMBLrel.
                                                              (TrEMBLrel.
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                                                                                        PRELIMINARY;
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Chordata; Craniata;
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30.5%;
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Last sequence up
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Pred. No. 4.
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Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC32;
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ea; Pipidae;
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                                    update)
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Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               881;
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125

SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 184

Best Local S
Matches 78

Similarity 34.8 78; Conservative

34.8%;

Score 306; Pred. No. 5

DB 6; 1 5.6e-19; 1es 92;

Length 581;

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Mismatches

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Best Local S
Matches 81
                 CHAIN
SEQUENCE
                                                                              BIGNON C., DJIANE J.;
Submitted (JAN-1998) to t
EMBL; AF041257; AAB96795.
                                                                                                                                         and genomic analysis reveal that the two forms arise by alternative splicing mechanisms in ruminants and in rode J. Mol. Endocrinol. 19:109-120(1997).
                                                                   PFAM; PF00041; fn3;
                                                                                                                                                                                                                                                                              Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata;
Eutheria; Cetartiodactyla; Ru
                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TIEMBLIE1. 06,
01-JUN-1998 (TIEMBLIE1. 06,
01-MAY-1999 (TIEMBLIE1. 10,
PROLACTIN RECEPTOR LONG FORN
                                                                                                                                                                                                                                                                                                                                                                         046561;
                                                                                                                                                                                                                          SEQUENCE FROM N.A. WEDLINE; 98001468.
                                                                                                                                                                                                                                                                                                                                                                                       046561
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EMBL; S78505; AAB34470.1; -.
FFAM; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                   Caprinae; Ovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     178
                                                                                                        EQUENCE FROM N.A.
                                                                                                                                                                                                              IGNON C., BINART N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLVQVRCKP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YFYQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTEFKILSLHPGQK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLELAV-EVKQPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLMHECPDYITGGP 59
                                                                                                                                                                                    and short forms of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                             Cetartiodactyla;
                 581 AA;
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                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
581
65235 >
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                                                                                                                                                                                                                                                                           ca; Craniata; Vertebrata; Mammalia;
Ruminantia; Pecora; Bovoidea; Bovi
              POTENTIAL.
PROLACTIN R
6792A7C7
                                                                                           EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                   ovine
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                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Mismatches
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                                                                                                                                                                                                           SCHULER L.A.,
                                                                                                                                                                                prolactin receptor: cDNA cloning
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No. 3.4
                                                                                                                                                                                                                                                                                                                                                                                    581
              RECEPTOR 7 CRC32;
                                                                                                                                                                                                                                                                          Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  203
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                                                                                                                                                                                                           P.A.
                                                                                                                                                                                                                                                                          Bovidae;
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Best Local
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 10, Last annotation update)
PROLACTIN RECEPTOR (FRAGMENT).
                                                                                 093404
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EMBL; AF027403; AAB83999.1; -.
PFAM; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROLACTIN RECEPTOR SHORT FORM
                                                                                                                                                            211 --- DHGYWSEWSPESSIQIP 227
                                                                                                                                                                                           323
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                                                                                                                                                                                                                                                                                                                                                                                      151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHULER L.A., NAGEL R.J., GAO J., Prolactin receptor heterogeneity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovinae; Bos.
                                                                                                                                                                                                                                                                                          99
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-JAN-1998 (TrEMBLrel. 05,
-NOV-1998 (TrEMBLrel. 08,
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                                                                                                                                                                                                                   .DVKSGWFIIQ--YEIRLKPEKATDWE-THFTLKQTQLKIFNLYPGQKYLVQIRCKP----
                                                                                                                                                                                                                                                  D-----FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIY 322
                                                                                                                                                                                                                                                                                  YVITVNAINOMGISSSDPLYVHVTYIVEPEPPANLTL-ELKHPEDRKPYLWIKWSPPTMT 157
                                                                                                                                                                                                                                                                                                                YEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWV--SPPALK 267
                                                                                                                                                                                                                                                                                                                                                KETFTCWWEPGADGG--LPTNYTLTYHKEGETLIHECPDYKTGGPNSCYFSKKHTSIWKM 98
                                                                                                                                                                                                                                                                                                                                                                             MKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHI-PKDLALFTP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                             SRLLNTSTLALALANLNGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRN 150
                                                                                                                                                                                          GSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                  SRVVFILLLFLSVSLLNG---QS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SILNGQS-----PPEKPKLIKCRSPGKETFTCWWEPGADGG--LPINYTLTYRKEGETLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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296 AA;
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                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33854 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 302.5; DB b;
Pred. No. 4.7e-19;
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Last annotation update)
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                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8B40CCD8 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                               346 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata; Mammalia;
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01-JUN-1998 (TIEMBLIEL 06, Created)
01-JUN-1998 (TIEMBLIEL 06, Last seq
01-MAY-1999 (TIEMBLIEL 10, Last ann
                                                             N
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                   DOUGLAS D.A., SONG J.-H., HO Submitted (OCT-1997) to the EMBL; AF029294; AAB88899.1; FFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                          Mustela vison (American mink).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHIRAISHI K., MATSUDA M., MORI T., TETSUYA H.;
"Expression of prolactin and cortisol receptor gene in early-life
stages of tilapia (Oreochromis mossambicus).";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF080247; AAC31825.1; -.
PFAM; PF00041; fn3; 2.
NON_TER 346 346
SEQUENCE 346 AA; 39203 MW; 1EBA63B9 CRC32;
                                                                                                                                                                                                                                                                                                                                                             Eutheria; Carnivora; Fissipedia;
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                         PROLACTIN RECEPTOR (FRAGMENT).
                            219 RLGSARSDYLTLDVLDVYTTDPPPDVHVSRVGGLEDQLSVRWVS--PPALKDF---LFQA 273
                                                                                                  160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 TYLIQVRCKP------DHGFWSEWSSTSYVKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 WPFLRVSW-EPPHKADTRSGWITLIYELRVKLEDEESEWE-NHAAGQQKMFNIFSLRSGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 PEKPFNISCWSRNWKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oreochromis mossambicus
60 EMGSSSSDPRYVTLTYIVEPDPPVNLSL-ELKQPEDKKTYLWIKMYPPTLVDVRSGWLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 VYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neopterygii; Teleostei;
                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29
                                                           PGEDGG--LPTKYTLTYHKEGETTTHECPDYITSGPNSCYFNKKHTSIWTMYIITINATN 59
                                                                                          PGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHI-PKDLALFTPYEIWVEATN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHIPK-DLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQ- 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CFFNKNDTLIWVSYNITVVATNALGKTYSDPVDIDVVYIVKPHPPEKLEVT---VMKDQG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGKPTEITCRSPEKETFTCWWKPGSDGG--LPTTYALYYRKEGSDVVHECPDYHTAGKNS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LSVRWVSPPALKDF---LFQAKYQIRYRVED-SVDWKVVDDVSNQTSCRLAGLKPGT 308
                                                                                                                             1 Similarity
61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                         217
217 AA;
                                                                                                                                                                                                                                                                                                                                                                             Metazoa; Chordata;
                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                       217
                                                                                                                                          10.1%; Score 234.5; DB 32.3%; Pred. No. 3.1e-13
                                                                                                                                                                                                         24850 MW;
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rdata; Craniata; Vertebrata; Actinopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cichlidae; Tilapia.
                                                                                                                             30;
                                                                                                                                                                                                                                                                                                 HOUDE A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 268.5; DB 13; pred. No. 5.8e-16; 28; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence up
                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Mammalia;
ia; Mustelidae; Mustela.
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                                                                                                                             Mismatches
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Best Local (
                                                                                                                                               Ovis aries (Sheep).

Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata;

Eukaryota; Metazoa; Chordata; Ruminantia; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-1997) to t)
EMBL; Y14753; CAA75048.1;
PFAM; PF00041; fn3; 1
SEQUENCE 198 AA; 22652
                                            STRAIN-M22/80; TISSUE-ANTERIOR PITUITARY; TORTONESE D.T., BROOKS J., INGLETON P., M SUBMILTED (JAN-1997) to the EMBL/GenBank/EMBL; Y10578; CAA71597.1;
                                                                                                                                                                                                      01-MAY-1997 (TIEMBLIE) 03, Created)
01-MAY-1997 (TIEMBLIE) 03, Last seq
01-MOV-1998 (TIEMBLIE) 08, Last ann
PROLACTIN RECEPTOR (FRAGMENT).
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Eutheria; Cetartiodactyla; Ru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cervus elaphus nelsoni (American elk)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              018985
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NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                   297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 DGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYG 182
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1-NOV-1998
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                                                                                                             EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     189
                                                                                                                                            aprinae; Ovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QDNTCEEYHTVGPHSCHI-PKDLALFTPYEIWVEATNRLGSARSDYLTLDVLDVYTTDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                ANLTL-ELKHPEDRKPYLWIKWFPPTLTDVKSGWFMIQYEIRLKPETATDWE-HDDLHPP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIHECPDYKTGGPNTCYFSKKHTSIWKIYVITVNAINQMGVSSSDPLYVDVTYIVEPEPP
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                                                                                                                                                                                                                                                                                                                                                                                                 TSCR 300
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                                                                                                                                                                                                                                                                                                                                                                     TSSR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDVHVSRVGGLEDQLSVRWVS--PPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 296
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                               PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
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(TrembLrel. 08, Last ann
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                                                           EMBL/GenBank/DDBJ
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l; Mismatches
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                                                                                                                                                        Pecora;
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                                                                                                                                                                       Vertebrata; Mammalia;
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Pecora; Cervoidea; Cervidae;
                                                                            MCNEILLY A.
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                                                                                                                                                        Bovoidea;
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                                                                                                                                                      Bovidae;
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Best Local S
Matches 58
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Best Local
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088507
                                                                                                                                                                                                                                                                                             SEQUENCE
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Mus musculus (Mouse),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eurtheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           KOJIMA T., HASEGAWA M., KIKUCHI Y., NOMURA H.;
"Mouse homolog of human ciliary neurotrophic f
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ
EMBL; AP068615, AAC25711.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998
01-WAY-1999
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                                                                                                                                                                                                                                                                                                                                                                     FAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASEDA M., YAGUCHI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 GETFLHINYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGS
                                                       116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 RIKPEKATOWE-THFAPKLTQLKIFNLYPGQKYLVQIRCKP----
 164
                                                                                  146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 FIQIP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 AASTP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 ARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQI
                                                                                                                                         87
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                                                                                                                                                                                            30 CVLGVPRGGSGAHTAVISPODPTLLIGSSLQATCSIHGDTPGATAE---GLYWTLNGRRL
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CHI-RYMHLFSTIKYKVSISVSNALGH-NTTAITFDEFTIVKPDPPENVVARPVPSNPRR
                                                                                CWSRNM-KDLTCRW-----TPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS 197
                                                                                                                                        PSELSRILINTSTIALALANLINGSRQQSGDNLVCHARDGSILAGS-CLYVGLPPEKPFNIS
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                          CHIPKDLALFT - - PYEIWVEATURLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQ
                                                                                                            APD --- LINGSQLILRSLELGHSGLYA ----- CFHRDSWHLRHQVLLHVGLPPREPV-LS
                                                                                                                                                                  CCAVLAAAAAVYTQKHSPQEAPHVQYERLGADVTL----PCGTASWDAAVTWRVNGTDL
                                                                                                                                                                                                                          1 Similarity
97; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
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                                                                                                                                                                                                                                                                                               372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                               A.
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RECEPTOR ALPHA PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created
                                                                                                                                                                                                                                        Score 226; DB 11;
Pred. No. 3.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 226.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                            ALPHA
                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CILIARY NEUROTROPHIC FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88A05AB1 CRC32;
                                                                                                                                                                                                                                                                                             9A40FE12 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAKATA Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68;
                                                                                                                                                                                                                                                                                                                                                                                                                        factor receptor.";
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                                                                                                                                                                                                                                                   Length 372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TULIN E.
                                                                                                                                                                                                                                                                                                                         RECEPTOR
                                                                                                                                                                                                                          74;
                                                                                                                                                                                                                        Gaps
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                                                                                                                                        145
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 221
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ESULT 12
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Best Local :
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                                            01-MAY-1997
01-NOV-1998
                                                                          01-MAY-1997
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01-MAY-1997
01-NOV-1998
                                                                                                       P97378
                                                                                                                                                                                                                                     247
                                                                                                                                                                                                                                                                                              198
                                                                                                                                                                                                                                                                                                                                                141 VACTWERGR -- DTHLYTEYTLQLSGPKNLTWQKQCKDIYC - DYLDFGINLTPESPESNFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00041;
SEQUENCE 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-1996) to the EMBL/GenBank/DDBJ EMBL; U64198; AAB36675.1; -.
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                              NTERLEUKIN
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                                                                                                                                                                                                                                                                                                                          201
                                                                                                                                                                                                                                                                                                                                                                                   154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.

RESKY D.H., YANG H., MINETTI L.J.,

ATELY M.K., GUBLER U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lomo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           utheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 CEP----RGGEPS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 LLIGSSLQATCSIHGDTPGATAEGLYWTL-----
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musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 RECEPTOR BETA2.
                                                                                                                                                                                                   IYGSKKAGIWSEWSHPTAASTPRSERPG 348
                                                                                                                                                                                                                                                                                                                                                                             LTCRWTPGAHGETFLHTNYSLKY----KLRWYGO--DNTCEEYHTVG------PHSCHI 200
                                                                                                                                                                             - X.1
                                                                                                                                                                                                                                                          VSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFG
                                                                                                                                                                                                                                                                                       AK------VTAVNSLGSSSSLPSTETFLDIVRPLPPWDIRIKFQKASVSRCTLYW
                                                                                                                                                                                                                                                                                                                  PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRW 260
                                                                                                                                                                                                                                                                                                                                                                                                                                     NTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMK-D 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILLGSTVNITCSL-
                                                                                                                                                                                                                                                                                                                                                                                                                GTTLFVCKLACINSDEIQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK-----DNEIGTWSDWSVAAHATPWTEEPRHLTTEAQAPETTTSTTSSLAPPPTTKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEVIWOTPSIWPDPESFPLKFFLRYRPLILDQWQHV-ELSDGTAHTITDAYAGKEYIIQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 25.6
34; Conservative
                                                                                                                                                                          -KGSWSDWSESLRAQTPEEEPTG
                           ' (TrEMBLrel. C') (TrEMBLrel. C') (TrEMBLrel. C') (TrEMBLrel. C') N 12 RECEPTOR,
                                                                                                                                                                                                                                RDEGLVLLNRLRYRPSNSRLWNMVNVTKAKGRHDLLD:
                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97134 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.4%;
                   . 03,
. 03,
. 08, L
. BETA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
                        Last sequence update)
Last annotation update)
TA 2 (IL-12 RECEPTOR BETA2).
                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 217.5; DE
Pred. No. 6e-11;
                                                                                                    PRT;
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                                                                                                                                                                                                                                CKPFTEYEFQI-SSKLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            862;
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Q16542
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Best Local Similarity 25.3
Matches 96; Conservative
                                                                                                                                                                                                                                                                             Q16542; Q14636;
Q16542; Q14636;
01-NOV-1996 [TIEMBLIE]: 0
01-NOV-1996 [TIEMBLIE]: 0
01-NOV-1998 [TIEMBLIE]: 0
                                                                                           CHEREL M., SOREL M., LEBEAU B., DUBOIS MINVIELLE S., JACQUES Y.;
"Molecular cloning of two isoforms of hematopoletic cytokine interleukin-11. Blood 86:2534-2540(1995).
                                         SEQUENCE FROM N.A.
VAN LEUVEN F., STAS L.,
Submitted (SEP-1995) to
                                                                                                                                                                                                                 Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
PRESKY D.H., YANG H.,
GATELY M.K., GUBLER U.
                                                                                                                                                                   EDLINE; 95399754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-1996) to the EMBL; U64199; AAB36676.1; MGD; MGI:1270861; IL12RB2.
EQUENCE OF 3-390 FROM N.A. ISSUE-PLACENTA;
                                                                                                                                                                                                                                                                      NTERLEUXIN-11
                                                                                                                                                                                                                                                                                                                                                                                                                                          330 WSEWSHPTAASTPRSERPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 VLNQLRYQPLNSTSWNMVNATNAKGKYDLRDLRPFTEYEFQI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 AKYOIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSK---KAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 K--VTYLKTNYTLQLS----GPNNLTCQKQCFSDNRQNCNRLDLGINLSPDLA-ESRFIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 CKLNCSNSQKKPPVPVC------GVEISVGVAPEPPQNISCVQEGENGTVACSWNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 ANLNGSRQQSGDNL-VCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMK-DLTCRWTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 WVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 CSLNPKQGCSHYPSSNELILLKFVNDVLVENLHGKKVHDHTGHSSTFQVTNLSLGMTLFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 CSIH-----GDTPGATA------EGLYWTLNGRRL-----PSELSRLLNTST-LALAL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAQTVRECSLALLELEMWILIKANIDVCKLG-----TVTVQPA-PVIPLGSAANIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 VAOSARRPPRPLSSLWSPLLL-----CVLGVPRGGSGAHTAVISPODPTLLIGSSLOAT 62
                                                                                                                                                                                                                                                                                                                                                                                                                WSNWSESLRTRTPEEEPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AHGETFLHTNYSLKYKLRWYGQDN-TCE-EYHTVGDHSC-----HIPKDLALFTPYEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98196 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MINETTI L.J., CHUA A.O., NABAVI N.,
                                                                                                                                                                                                                                                                                 82£
                                       HILLIKER C., MIYAKE Y., the EMBL/GenBank/DDBJ d
                                                                                                                                                                                                                                                                                                                                                                                                                                            348
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                                                                                                                                                                                                                                                                                                             Created)
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Pred. No. 9.1e-11;
9; Mismatches 145;
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                                                   GOSSLER A.;
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Matches 89
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01-JAN-1998 (TIEMBLIEL 05, LAS
01-NOV-1998 (TIEMBLIEL 08, LAS
INTERLEUKIN-11 RECEPTOR ALPHA C
(IL-11RALPHA) (IL11RA1).
IL11RA1 OR IL11RA OR ETL2 OR ET
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EMBL; U32324;
EMBL; Z38102;
EMBL; U32323;
EMBL; Z46595;
                                                                                                                                  STRAIN-C57BL/6 X CBA; TISSUE-LIVER;
MEDLINE; 95045567.
HILTON B.A., RAICEVIC A., RAKAR S., H
HILTON D.J., HILTON A.A., RAICEVIC A., NICOLA N.A.,
"GOUGH N.M., BEGLEY C.G., METCALF D., NICOLA N.A.,
"Cloning of a murine IL-11 receptor alpha-chain; r
"Cloning of a murine IL-11 receptor alpha-chain; r
gpl30 for high affinity binding and signal transdu
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              NEUHAUS H., BETTENHAUSEN B.,
GUENET J.L., GOSSLER A.;
Dev Biol 166.831-810.1001.
                                                                  SEQUENCE FROM N.A.
STRAIN-BALB/C, AND C57BL/6;
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q64385;
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166:521-542(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                            (Mouse).
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CAA86224.1;
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                                             TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
HA CHAIN 1 PRECURSOR (NR1)
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                                          SIMON-CHAZOTTES
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, WILLSON T.A.;
requirement for
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Best Local Similarity 23.9%;
Matches 94; Conservative
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SEQUENCE FROM N.A.
STRAIN-BALB/C, AND
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CARBOHYD
SEQUENCE
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DOMAIN
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PFAM; PF00047; 1g;
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Biochem. J. 320:359-363(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BILINSKI P., HALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOSSLER A.;
Submitted (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
 312
                      347
                                                              289
                                                                                   212
                                                                                                                              155
                                                                                                                                                  183
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Two differentially expressed
                                                                                                                                                                                           123
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                                                                                                                                                                                                                                                           31
                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
TISSUE SPECIFICITY: WIDELY EXPRESED.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: PART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:107426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTAINS ONE IG-LIKE DOMAIN
                                                                                                                                                                     DGVSGGMVTLKLGFPPARP-EVSCQAVDYENFSCTWSPGQ--VSGLPTRYLTSYRKKTLP
                                                                                                                                                                                                                                    GDTPGATAEGLYWTLNGRRLPSELSRLLN--TSTLA--LALANLNGSRQQSGDNLVCHAR
                                                                                                                                                                                                                                                           GPPGVQYGQPGR-----PVMLCCPGVSAG-----
                    PGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKH 380
                                        TVEPIGLEEVITDAVAGLP----HAVRVSARDF-----LDAGTWSAWS-PEA-
                                                             VVDDVSNQ--TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSER
                                                                                  LOSILRPDPPQGLRVESVPGYPRRLHASWTYPASWRRQPHFLL--KFRLQYRPAQHPAWS
                                                                                                     VLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALK---DFLFQAKYQIRYRVEDSVDWK
                                                                                                                            GAESQRESPSTGPWPC--PQDPLEASRCVVHGAEFWSEYRINVTEVNPLG-ASTCLLDVR
                                                                                                                                                QDNTCEEYHTVGPHSCHIPKD-----LALFTPYEIWVEATNRLGSARSDVLTLD
                                                                                                                                                                                          DGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYG
                                                                                                                                                                                                                                                                              GPVAQSARRPPRPLSSLWSPLLLCVLGVPRGGSGAHTAVISPQDPTLLIGSSLQATCSIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X94162; CAA63873
X94163; CAA63873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X74953; CAA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TO IL-11 WITH LOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FEB-1995)
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                                                                                                                                                                                                                -VSWFRDGD-----SRLLQGPDSGLGHRLVLAQVDSPDE-
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WGTPSTGPLQDEIPD---WSQGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                              432
367
393
102
127
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                                                                                                                                                                                                                                                                                                                                                         46655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                         MW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR FOR
                                                                                                                                                                                                                                                                                                      <u>5</u>1,
                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL POTENTIAL). CYTOPLASMIC (POTENTIAL). IG-LIKE CZ-TYPE DOMAIN. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFFINITY,
                                                                                                                                                                                                                                                                                                  Score 208.5; DB 11;
Pred. No. 1.5e-10;
il; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERLEUKIN-11
                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                         CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAMILY OF
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C
                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            databases
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                                                                                                                                                                                                                                                                                                     Indels
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TRANSDUCE
                                                                                                                                                                                                                                                                                                                        Length 432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       fold;
                                                                                                                                                                                                              -GIYVCQIL
                                                                                                                                                                                                                                                                                                     113;
                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
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                                                                                                                                                                                                                                                                                                  Gaps
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CONFLICT
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                                                                                                                                                                                                                                                     CANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sceptor alpha-chain and a related :
Biol. Chem. 271:13754-13761(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NWO differentially expressed interleukin-11 receptor genes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us musculus (Mouse).
Ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Utheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAIN-CD1; TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tructural analysis of the gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEINE; 96278810.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIN-CD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONTAINS ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISSUE SPECIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11CS 40:387-394(1997).

PART OF THE RECEPTOR FOR INTERLEUKIN 11.

TOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320:359-363(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR LOCATION: TYPE I MEMBRANE PROTEIN.
HETERODIMER OF AN ALPHA AND A BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ll receptor alpha chain 2 precursor (Illira2) (INTERLEUKIN-11 RECEPTOR BETA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ILllRa2) with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J., BROOK-CARTER P.T., BEGLEY C.G.,
a second murine interleukin-11 receptor
8.7%; Score 201; DB 11;
24.6%; Pred. No. 6.9e-10;
ative 49; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TY: WIDELY
                                                                                                         46721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WILLSON T.A., BEGLEY C.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TO THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                                                                                                                                                                           Glycoprotein; Immunoglobulin fold; Signal.
                                                                                                         MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOINED
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                                                                                                                                                                                                                                                            INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2.
                                                                                                                                                                                                   YTOPLASMIC (POTENTIAL).
                                                                                                  -> P (IN CAA63872).
-> L (IN CAA63872).
C4FD7DEC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restricted pattern of expression.";
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Query Match 8.7 Best Local Similarity 24.6 Matches 97; Conservative

Length 432; Indels 100;

Gaps

20;

	LQDEIPDWSQGHGQQLEAVVAQEDSLAPARPSLQ 353	320	ઠ
	-RSERPGPGGGVCEPRGGEPSSGPVRRELK 371	343	Qy
319	TVEPIGLEEVITDTVAGLPHAVRVSARDFLDAGTWSAWS-PEAWGTPSTGL 31	270	문
343	VVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP	289	Ϋ́
269	LQSILRPDPPQGLRVESVPGTPRRLHASWTYPASWRRQPHFLLKFRLQYRPAQHPAWS 26	212	밁
288	232 VLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWK 28	. 232	VQ.
21	155 GAESORESPSTGPWPCPODPLEASRCVVHGAEFWSEYRINVTEVNSLG-ASTCLLDVR 21	155	ઠ
23	183 QDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLD 23	183	Ş
15	98 DGVSGGMYTLKLGFPPARP-EVSCQAVDYENFSCTWSPGQVSGLPTRYLTSYRKKTLP 15.	. 98	ઠ
18	DGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYG	123	VQ.
97	55TPVSWFRDGDSRLLQGPDSGLGHRLYLAQVDSPDEGTYVCQTL 97	5.5	망
12	67 GDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCHAR 12	67	δ
55	31 GPPGYQYGQPGRPVMLCCPGVSAG	įω	밁
66	เก		ν.

Search completed: September 16, 1999, 20:40:05

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RESULT
W55015
ID W5
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PT New isolated haemopoletin receptor - used for developing products pr for modulating proliferation, differentiation and survival of cells, PT for medulating proliferation, differentiation and survival of cells, PT e.g. neuronal cells

PT e.g. neuronal cells

CC claim 16; Page 90-92; 182pp; English.

CC Interaction between the novel HR and a ligand facilitates proliferation, cells and survival of a wide variety of cells. The HR and it's CC differentiation and survival of a wide variety of cells. The HR and it's CC different cells and tissues in vitro and in vivo in an array of CC different cells and tissues in vitro and in vivo. They can be present in CC cens the composition of the products can also be used for detection and diagnosis, CC e.g. for cancers or predisposition to cancers, or for drug screening.

SQ Sequence 155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Sir
Matches 155;
Homo sapiens.
W09811225-A2.
19-MAR-1998.
                                                                     Human.
                                                                                 Amino acid sequence of clone Haemopoletin receptor; cell cell survival; therapeutic;
                                                                                                                                                                                                                   W55015
                                                                                                                                                                   29-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                      121 PGEQPPQHRTLLSKHRTRGSCPRADGVRREVRGSG
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WPI; 98-260970/23.
                                                                                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS
(DZIE) DZIEGLEWSKA H E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel haemopoietin receptor NR6.3 protein.
Haemopoietin receptor; cell proliferation; cell dif.
cell survival; therapeutic; neuronal proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel haemopoietin
Haemopoietin recept
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                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                               PGEOPPOHRTLLSKHRTRGSCPRADGVRREVRGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPV
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                                                                                                                                                                                                           standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                            (first entry)
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sh A, Nicola NA, 1
                                                                                           ione HFK-66 encoding human NR6.
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                                                                                      proliferation;
neuronal proli
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W23155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 864; DB 1;
Pred. No. 1.9e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Å
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                                                                        proliferation; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n DJ, Kikuchi Y,
Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell differentiation; ca
feration; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Human
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Matches
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01-MAY-1998; US-074721.

13-FEB-1998; US-074721.

01-MAY-1997; US-045287.

01-MAY-1997; US-850030.

13-FEB-1998; US-023890.

(ZYMO ) ZYMOGENETICS INC.

Adams RL, FOSTET DC, Gilbert T,

Lok S, Presnell SR, Whitmore TI

WPI; 99-034662/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; Page 102-104; 182pp; English.

The NR6 protein is a novel Haemopolettin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis,
                                                  Claim 1; Page 89-90; 55pp; English.
The present sequence represents a Zcytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered down-regulate the effects of a growth and/or maintenance factor thyroid, heart, and skeletal muscle for example to lessen the elements.
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W09849307-A1.
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maintenance factor; thyroid; heart; skeletal muscle
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T, Maeda M, Nash A,
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GTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPV RRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVGKLGEACVGGKGAEEERD Query Match Best Local S Matches 116

Similarity

73.1%; 76.8%;

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Matches 116; Conser
                  thyroid, heart, and skeletal muscle for example to lessen the of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the pres and integrity of the Zcytor5 gene on chromosome 19. Antibodies anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.
                                                                                                                                                                                                                                                              The present sequence represents a 2cytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered down-regulate the effects of a growth and/or maintenance factor in
                                                                                                                                                                                                                                                                                                                                                                                    New mammalian cytokinin-like receptor Zcytor5 - useful for, down-regulating Zcytor5 natural ligands or detecting cardiot in blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zcytor5; cytokinin-like receptor; down-regulation; growth
maintenance factor; thyroid; heart; skeletal muscle; cardi
cardiac pathology; heart enlargement; 2cytor5 ligand; vari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 99-034662/03
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L, Foster DC, Gilbert T, C, Foster DC, Whitmore TE;
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Pred. No. 1.5e
0; Mismatches
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No. 1.5e-58;
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Best Local Sim
Matches 116;
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17-MAR-1999 (first entry)
17-MAR-1999 (first entry)
Human Zcytor5 variant.
Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophi
maintenance factor; thyroid; heart; sveletal muscle; variant.
                                                                                       W70849 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mammalian cytokinin-like receptor
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Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
WDI: 99-034662/03
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maintenance factor; thyroid; heart; skeletal muscle
cardiac pathology; heart enlargement; 2cytor5 ligar
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                                                                                                                                                                                                                                                                                                                                73.18;
Similarity 76.88;
16; Conservative
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Pred. No. 1.5e-58;
0; Mismatches 2;
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cting cardiotrophin-1
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             cardiotrophin-1;
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Best Local :
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                                                                      (2YMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
                                                                                                            01-MAY-1997; US-850030
13-FEB-1998; US-023890
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01-MAY-199
                                                    New mammalian
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Human Zcytor5 variant.
Zcytor5; cytokinin-like re
                                       down-regulating
                                                              WPI; 99-034662/03
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W09849307-A1
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WO9849307-A1.
05-NOV-1998.
01-MAY-1998;
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                                                                                                                                                                                                                                                                                 W70850 standard; Protein;
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01-MAY-1997; US-850030
13-FEB-1998; US-023890
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Lok S, Presnell SR, Whitmore
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116; Conserva
                                                                                                                                                                                                                    cytokinin-like receptor; down-regulation; nce factor; thyroid; heart; skeletal musch
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97; US-045287
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                                 cytokinin-like receptor Zcytor5 g Zcytor5 natural ligands or det
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55pp; English.
represents a ?
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                                useful for, e.g.tecting cardiotrophin-1
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cardiotrophin-l
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Ecytor5 variant

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Matches 116
   Query Match 73.
Best Local Similarity 76.
Matches 116; Conservative
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13-FEB-1998; US-074771.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
                                                                                                  Claim 1; Page 96-97; 55pp; English. Zcytor5 variant protein. Zcytor5 The present sequence represents a Zcytor5 may be administered to is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.
                                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC.
Adams RL, Foster DC, Glibert T, Jelmberg Lok S, Pressell SR, Whitmore TE;
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maintenance factor; thyroid; heart; skeletal muscle; cardiotro
cardiac pathology; heart enlargement; Zcytor5 ligand; variant.
                                                                                                                                                                                                                                                                                                                                  New mammalian cytokinin-like receptor Zcytor5 - usefo
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Human Zcytor5 variant.
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76.8%;
                  73.1%;
 Score 631.5;
Pred. No. 1.5
0; Mismatches
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No. 1.5e-58
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cting cardiotrophin-1
                                Length 389;
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                                                                                                                                                                         Query Match
Best Local S
Matches 116
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01-MAY-1998; U08865.

13-FEB-1998; US-074721.

01-MAY-1997; US-045287.

01-MAY-1997; US-850030.
                                                                                                                                                                                                                                             The present sequence represents a Ecytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g. down.regulating Zcytor5 natural ligands or detecting cardiotrophin-l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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hes 116;
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                             PGEQPPQHRTLLSKHRTRGSCPRADGVRREV
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                                                                                                               GTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPV 326
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HRTRGSCPRADGARREV
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76.8%;
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Pred. No. 1.5e-58;
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RESULT W70853 ID W7 AC W7

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Best Local Similarity 76.0
Matches 116; Conservative
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13-FEB-1998; 1
01-MAY-1997; 1
01-MAY-1997; 1
13-FEB-1998; 1
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01-MAY-1998; U08865.

13-EB-1998; US-0747;

01-MAY-1997; US-0452;

01-MAY-1997; US-8500
L3-FEB-1998; US-023890
(ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T,
LOK S, Presnell SR, Whitmore TE;
WPI; 99-034662/03
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                                                                                                                                                                                                                                                                                                                                 Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal_muscle; cardiotrophi
                                                                                                                                                                                                                                                                                                                      cardiac pathology;
                                                                                                                                                                                                                                                                                                                                                                             Human Zcytor5 variant
Zcytor5; cytokinin-li
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Adams RL, Foster DC, Gilbert T,
Lok S, Presnell SR, Whitmore TE;
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                                                                                                                                  US-074721.
US-045287.
US-850030.
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                                                                                                                                                                                                                                                                                                                   oid; heart; skeletal :
enlargement; Zcytor5
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Pred. No. 1.5e-58;
0; Mismatches 2;
                                            Jelmberg AC,
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The present sequence represents a Zoytor5 variant protein. Zcytor5 (CC is a cytokinin-ilke receptor. Soluble Zcytor5 may be administered to CC down-regulate the effects of a growth and/or maintenance factor in CC of cardiotrophin-1 on cardiac pathologies, so preventing heart CC enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the CC comprising Zcytor5 DNA or RNA can be used to determine the probe CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the Integrity of the Zcytor5 gene on chromosome 19. Antibodies and the CC anti-idiotypic antibody could be used to purify Zcytor5 and the Zcytor5 ligand effects.
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Best Local :
The present sequence represents a Zcytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
                                                                                                                                                           Claim 1; Page 87-88; 55pp;
                                                                                                                                                                                                     New mammalian cytokinin-like
                                                                                                                                                                                                               (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
WPI; 99-034662/03.
                                                                                                                                                                                         down-regulating
                                                                                                                                                                                                                                                                                                                                                                                  cardiac pathology;
                                                                                                                                                                                                                                                                                                                                                                                             2cytor5; cytokinin-like receptor;
maintenance factor; thyroid; heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                W70844 standard; Protein; 389
                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAR-1999 (first
                                                                                                                                                                                                                                                                            .3-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTVYEYQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRELKOFLGWLKKHAYCSNLSFRLYDOWRAWMQKSHKTRNQ--
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                                                                                                                                                                                       Zcytor5
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                                                                                                                                                                                                                                                                                                                                                                                   heart
                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
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                                                                                                                                                                                                                                                                                                                                                                                  enlargement;
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                                                                                                                                                            English
                                                                                                                                                                                                                            TE,
                                                                                                                                                                                receptor Zcytor5 - useful for, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 631.5; DB 1
Pred. No. 1.5e-58;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor Zcytor5 -
cal ligands or dete
                                                                                                                                                                                                                                         Jelmberg AC,
                                                                                                                                                                                                                                                                                                                                                                                            down-regulation; g
t; skeletal_muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
                                                                                                                                                                                                                                          Lehner
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cardiotrophin-1
                                                                                                                                                                                                                                                                                                                                                                                       iotrophin-1;
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                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                 The present sequence represents an allelic varaint of protein designated Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance effect in thyroid, heart, and skeletal muscle for example to lessen the enlargement. Zcytor5 could be used to detect cardiotrophin-l in cardiac pathologies, so preventing heart blood, and to discover other possible Zcytor5 ligands. A probe and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and the presence anti-idiotypic antibody could be used to purify Zcytor5 and the sequence 425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams RL,
Lok S, Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-1998.
01-MAY-1998; U08865
13-FEB-1998; US-074
     404
                                                                                                                   303
                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                       down-regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zcytor5; cytokinin-like recept
maintenance factor; thyroid; h
                                121
                                                           363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiac pathology; heart enlargement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W70861 standard;
                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PSDB; V70895
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                                                                                                                         1 GTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
                                                                 RRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVGKLGEACVGGKGAEEERD 120
                                                   RRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQ
                                                                                                       GTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPV
                          PGEQPPOHRTLLSKHRTRGSCPRADGVRREV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99-034662/03.
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                                                                                                                                                                        116; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPV 326
                                                                                                                                                                                                                                                                                                                                                                                                            1; Page 71-72; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RL, Foster DC, Gilbert
Presnell SR, Whitmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      cytokinin-like receptor
ng Zcytor5 natural ligand
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HRTRGSCPRADGARREV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *HRTRGSCPRADGARREV 384
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76.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      natural ligands
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                                                                                                                                                                  Score 631.5;
Pred. No. 1.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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Pred. No. 1.5e-58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zcytor5
                                                                                                                                                                               1.6e-58;
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                                                                                                                                                                                            Length 425;
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                                                                                                                                                             Gaps
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                                                                                                          362
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel haemopoletin receptor NR6.2 protein. Haemopoletin receptor; cell proliferation; cell survival; therapeutic; neuronal proli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W55012 standard; Protein; W55012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     different texts and transcribed for modulating neuronal proliferation, differentiation, and diagnosis, and survival. The products can also be used for detection and diagnosis, and servival are products can also be used for detection and diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The haemopoletin receptor (HR) NR6.1 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in the process of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for modulating proliferation, e.g. neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 RRELKOFLGWLKKHAYCSNLSFRLYDOWRAWMOKSHKTRNOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; V27140
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11-SEP-1996; AU-002246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (o)ima T, Maeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alexander
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RRELKQFLGWLKKHAYCSNLSFRLYDQWRAWWQKSHKTRNQV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DZIE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      μ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102;
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Her W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
T, Maeda M, Nash A, Nicola NA, Rakar S, Willso
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sceptor; cell proliferation;
therapeutic; neuronal proli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 577; DB; Pred. No. 8.2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; I
8.2e-53;
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19-MAR-1998. 11-SEP-1997; G02479. 11-SEP-1996; AU-002246. (AMRA-) AMRAD OPERATIONS PTY LTD. (DZIE/) DZIEGLEWSKA H E.

Chang Alexander

Maeda M, W, Fabri

A H E.

L, Farley A, Hli

A h A, Nicola)

Hilton

98-260970/23)B; V27141.

Prove isolated haemopoletin receptor - used for developing products for modulating proliferation, differentiation and survival of cells, e.g. neuronal cells.

The e.g. neuronal cells

Claim 15; Page 84-87; 182pp; English.

The haemopoletin receptor (HR) NR6.2 is a form of the novel HR NR6.

Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, sequence 425 AA;

Sequence 425 AA;

Search completed: September 17, 1999, 03:08:14 Job time: 305 sec

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Perfect score:
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US-07-797-556-6
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US-08-148-910-12
US-08-448-937A-12
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US-08-438-439C-7
                            US-07-943-843-6
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(without alignments)
28.357 Million cell updates/sec
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US-08-660-963-13
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Best Local :
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Patent No.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 12-JUN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: O'Shaughnessy, Brian I
REGISTRATION NUMBER: 32,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-824-8000
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ADDRESSEE: POPHAM, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MOLECULAR CLONING TITLE OF INVENTION: MOLECULAR CLONING GROWTH HORMONE REL NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Thorner, Michael O.
APPLICANT: Gaylinn, Bruce D.
APPLICANT: Horikawa, Reiko
APPLICANT: Lyons Jr., Charles
308 QVGLRCCVLGPGRQLP----LLVDHQ 329
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                                                 GFCDRLSFRDHDQLQLAAGRSCVPDLPLSLHIAQHKEGLLVAGSRCLGASSALHQHVGGL 307
                                                                                                     HPGRSQEAPLPQELHPHPAVHHLYPQGGSCVPEGRHPLSPGEHGPLQ-----LLHCPVQ
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US-08-419-652-7

US-08-822-262-1

PCT-US95-00670-4

US-08-205-018-2

US-08-395-580-2
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Ann
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              Daniel
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Pred. No.
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SHPTAASTP---RSER---PGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLS 81

FRLYDQWRAWMQKSHKTRNQVGKLGEACVGGKG-----

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Matches

Conservative

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Query Match
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April 10, 1992
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15-AUG-1991
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April 4, 1994
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Score 78;
Pred. No.
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-- RHRARHKAQPAHEAVEKE 995

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FELECOMMUNICATION INFORMATION:
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                                    STRANDEDNESS
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                                                           2237 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown, Martin, Haller & McClair
protein
internal
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04-APR-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MBER: 08/223,305
April 4, 1994
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                                                                                                                                                                                      04-APR-1988
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30-NOV-1990
                                   single
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20-FEB-1990
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BER: US_07/745,206
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PRIOR APPLICATION DATA:
                                                                                                           FILING DATE: 04-APR-1989 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/620,250
APPLICATION NUMBER: 30-NOV-1990
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                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/482,384 FILING DATE: 20-FEB-1990
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                                                                                                                                                                                                                                                                                                                                                                NEPLICATION NUMBER: 07/868,354
FILING DATE: ADT11 10, 1992
FOR APPLICATION DATA:
FOR APPLICATION NUMBER: US 07/745,206
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                                                                                                                                                 ATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Diskette
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Feldman, Daniel
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                                                                                                                                                                                 UMBER: US 07/603,751
04-APR-1989
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                                                                                                                                              WO PCT/US89/01408
                                                                                        US 07/176,899
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52516 (P519739)
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ECOMMUNICATION INFORMATION

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Local Similarity 23.2%;
les 33; Conservation
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                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 92101-2926
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                                                 PPLICATION NUMBER:
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                                                                                                                                                                      DATE: April 4, 1994
                                                                                                                                                                                                                                                                                                                                               California
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                                                                                                ION NUMBER:
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                                 30-NOV-1990
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15-AUG-1991
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57
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                                               US 07/620,250
US 07/482,384
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                                                                                           SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          978 ----RHRARHKAQPAHEAVEKE 995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 TLLSKHRTRGSC-PRADGVRRE 150
                                                                                 COMPUTER: IBM PC COMPUTED OPERATING SYSTEM: PC-DOS/MS-DOS
COPTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 FRLYDOWRAWMOKSHKTRNOVGKLGEACVGGKG---
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                              TORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER:
                                                                            APPLICATION NUMBER:
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                                                         12, 1995
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                                                                                                                                                                                                                                                                                                                          FIBROBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR-2 AND METHODS OF USE
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38,347
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Best Local Similarity
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                                                                                                               NFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:
US/08/808,550
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                                                                                                                                                               ELECOMMUNICATION INFORMATION
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                                                                                                                                                                              NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 104
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 26-FE
                                    STRANDEDNESS:
TOPOLOGY: 11:
                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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                                                                                ENGTH:
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New Jersey
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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N: 435
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26.4%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MMALIAN ENDONUCLEASE III AND LAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------CSNLSFRLY--DQWRA---WMQKSHKT--RN 100
                                                                                                                                                                                1049-1-001 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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ORGANISM:
US-08-808-550-42
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         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                         NFORMATION FOR SEQ ID NO:
                                                                                                        FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 297 amino acids
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 26-FEB-19
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 WMQKSHKTRNQVGKLGEACVGGKGAEEERDPGEQP 125
                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                               TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 TAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRA 90
                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esq., Dav
REGISTRATION NUMBER: 26
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 EARKSHSPVKRPRKAQRLRVAYEGSDSEKGEGAEP 73
                                                                                                                                                                                                                                                                                 ECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 SARMLTRSRSLGPGAG---PRGCREEPGPLRRR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08808550
                                                                                                                                                                                                                                                        201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                         Homo sapiens
                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              David A. Jackson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                   C-termina)
                                                                                                                                                                                                                                                                                                                                                                         26-FEB-1997
                                                                                                                                                 protein
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                                                                                                                                                                              single
                  25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Timothy P.

MAMMALIAN ENDONUCLEASE III AND
DIAGNOSTIC AND THERAPEUTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                   Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                        US/08/808,550
                   Score 71; DB
Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
    Mismatches
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                               DB 2;
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 Indels
26; Gaps
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2
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37 RSERPGPGGGVCEPRGGEPSSGPVRRELKÓFLGWIKKHAYCSNLSFRLYDOWRAWNOKSH 96

RSRSLGPGAG---PRGCREEPGPLRRR-

EAAAEARKSH 37

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                                                                                                                                                                                    RELEVANT RESIDUES US-08-026-138E-3
                                              밁
                                                                                                          Matches
                                                                                                                                     Query Match
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                                                                                                                                                                                                                                               UBLICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                              932 PT-TSGPRSCTPGPPGQP-SPSGWRPPGGGRTPLARRAP------ 969
87 QWRAWMQKSHKTRNQVGKLGEAC-----VGGKGAEEE---RDPGEQPPQ----HRTL 131
                                                                          30 PTAASTPRSERPGPGGGVCEPRGGEPSSG---PVRRELKQFLGWLKKHAYCSNLSFRLYD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 LECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDRESSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPVKRPRKAQRLRVAYEGSDSEKGEGAEP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTRNQVGKLGEACVGGKGAEEERDPGEQP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                         NDEDNESS:
                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08026138E
                                                                                                                                                                                                                                                                                           SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ION NUMBER
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                                                                                                                                                                                                                                Masayoshi MISHINA
                                                                                                                                                                                                                                                                             mouse
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                                                                                                                                                                                                                                                                                                                                      single strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                    -986
                                                                                                                                                                                                    IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOVEL PROTEINS AND GENES CODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP 303878/1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.50 inch, 1.44 MB storage
                                                                                                                                     Score 70.5;
                                                                                                                                                                                                                GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -4551
                                                                                                          Mismatches
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                                                                                                                                                                                                  CODING THE SAME
3: FROM 1 to 1239
                                                                                                                                     DB 1;
                                                                                                         42;
                                                                                                                                     Length 1239;
                                                                                                          Indels
                                                                                                         47;
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JS-07-814-964-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 LSKHRTRGSCPRAD 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MPUTER READABLE FORM:
NAME/KEY:
                            OTHER INFORMATION:
                                                                                                                                                    NAME/KEY:
                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                         QUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                ECOMMUNICATION INFORMATION:
                                                                                                                                       THER INFORMATION:
                                                                                                                                                                                                           EDIATE SOURCE:
                                                   AME/KEY:
                                                                                                                                                                                                                                                                                                                         MATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLICATION NUMBER:
                                                                                                            ME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRESSEE
                                                                                                                                                                                                                                               JULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                     NEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ICATION NUMBER:
                                                                                                                                                                                                                                                                            AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPPARPGPAQGRLSPTCPEHPAGTLGMRGGQCESGIRDRTSRPPERRALPERSL 1022
                                                                                                                                                                                           human SSRP (predicted)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plication US/07814964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                   Domain
440..496
                                                                                               Domain
512..534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Militia Drive
Domain
                                           Domain
539..6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ssigmann, John
                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy dis
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                                                                                                                                                                                                                                                                                                                         ID NO:
                                                                                                                                                                                                                                                                                                                                                                              NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein and Uses Therefor
                           /label= HMG-box
                                                                                /label= Basic I
                                                                                                                                       /label- Acidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 07/539,906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/07/814,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                             MIT-4787AAA
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Query Match
Best Local Similarity
Conservi
                                                                                                                                                     NFORMATION FOR SEQ ID NO:
                                                                        MOLECULE TYPE:
                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           644 SRGSSSKS 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584 IWKGMSKEKKEEWDRKAEDARRDYEKAMKEYEGGRGESSKRDKSKKKKKVKVKVKMEKKSTP 643
                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 -RGSCPRA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         529 RKSRKKP----VEVKKGKDPNAP-KRPMSAYMLWLNASREKIKSDHPGISITDLSKKAGE 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 RSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWL-----KKHAYCS--NLSFRLYD 86
                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Domain LOCATION: 661..709 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 623..640
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                           PUTER READABLE FORM:
                                                                                                                                                                                                                                                              ICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMA
                                                                                                                                                                                                                                                                                                                             UM TYPE:
                                                                                                                                                                                                                                                                                                                                                                 Chicago
: Illinois
RY: U.S.A.
                                                                                                                                                                                                                                                                     APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            60603
                                                                                                            AMINO ACID
                                                                                                                                                                                                         'AGENT INFORMATION: Feder, Scott B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/07745206A
                                                                                                                                                  ICATION INFORMATION:
E: 312-372-7842
FOR SEQ ID NO: 13:
                                                                                                                       1754 amino acids
                                                                                                                                                                                            /DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             135 S. LaSalle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams,
                                                                                                                                                                                                                                                                                                                 IBM PC compatible
                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESS:
                                                                                                                                                                                                                                                19910815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WMOKSHKTRNOVGKLGEACVGGKGAEEERDPGEOPPOHRTLLSKHRT- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steven
                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Calcium Channel Compositions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.9%;
21.9%;
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                                                                                                                                                                                                                                                            US/07/745,206A
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                                                                                                                                                                                                                                                                                                                                                                                                                        Tabin & Flannery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
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Pred. No. 17;
                Score 68.5;
Pred. No. 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                          DB 1; Length 1754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
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 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
59;
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Gaps
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                              IMMEDIATE SOURCE:
                                                            NAME/KEY: Domain
LOCATION: 440..496
OTHER INFORMATION:
NAME/KEY: Domain LOCATION: 512..534 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                906 AAEAQAPRAAGGTTGAAPR----RRRPSGS 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             816 PLVVELGRDGARGPVGGKARPEAAEAPEGVDPPRRHHR-
                                                                                                                                                                 ORGANISM:
                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 RRENT APPLICATION DATA:
                                                                                                                                                                                               ECULE TYPE
                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 PTAASTPRSERPGPGGGVCEPRGGEPSSG--PVRRELKQFLGWLKKHAYCSNLSFRLYDQ 87
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                            ELEPHONE:
                                                                                                                                                                              INAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                            GISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION DATA:
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                                                                                                                                                                                                                            amino acid
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                                                                                                                          human SSRP (predicted)
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                                                                                                                                                                                                                                           709 amino acids
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                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
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/label= Basic I
                                                              /label= Acidic
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; LOCATION: 661..709
; OTHER INFORMATION:
US-08-258-442-7
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Best Local Similarity
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                                                                                                                                                        CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        584 IWKGMSKEKKEEWDRKAEDARRDYEKAMKEYEGGRGESSKRDKSKKKKKVKVKMEKKSTP
                                                                                       TTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        529 RKSRKKP----VEVKKGKDPNAP-KRPMSAYMLWLNASREKIKSDHPGISITDLSKKAGE 583
                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 RSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWL-----KKHAYCS--NLSFRLYD 86
                                                         NAME: Fenton, Gillian REGISTRATION NUMBER:
                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                         SOFTWARE:
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LOCATION: 623..640
OTHER INFORMATION:
                                             EFERENCE/DOCKET NUMBER:
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                                                                                                           ASSIFICATION:
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               COMMUNICATION INFORMATION:
LEPHONE: 617-248-7000
                                                                                                                                                                                                                                                                                                                                     RESSEE
                                                                                                                                                                                                                                                          02109
                                                                                                                                                                                                                                                                                                    Boston
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617
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                                                                                                                                                                                 IBM PC compatible PC-DOS/MS-DOS
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                                                                                                                                    US/08/328,809
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                                                       36,508
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Pred. No. 1
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                                        COMPUTER READABLE FORM:
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 COMPUTER: IBM PC
OPERATING SYSTEM:
                         MEDIUM TYPE: Floppy disk
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LOCATION: 512..53.
OTHER INFORMATION:
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28; Conserv
                                                                                                                         SSEE:
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INFORMATION:
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                                                                                                San Diego
                                                                                 California
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                                                                                                                                      ENCE ADDRESS
                                                                                                                                                                                                                                                                                                       Application US/08311363
                                                                                                           1660 Union Street
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Feldman, Daniel
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623..640
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539..614
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                                                                                                                           Brown, Martin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        --WMQKSHKTRNQVGKLGEACVGGKGAEEERDPGEQPPQHRTLLSKHRT- 138
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PC-DOS/MS-DOS
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                                                                                                                                                                            Calcium Channel Compositions and
                                                                                                                        Haller & McClain
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Pred. No. 1
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WOLECULE TYPE:
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Best Local Similarity 22.0
Matches 33; Conservative
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PRIOR APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33.779

REGISTRATION NUMBER: 33.779
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPAX: (619)238-UUU2
NFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1754 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
906 AAEAQAPRAAGGTTGAAPR----RRRPSGS 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 63
FELECOMMUNICATION INFORMATION: (619)238-0999
                                        132 LSKHR-----TRGSCPRADGVRREVRGS 154
                                                                                                                                                                  816 PLVVELGRDGARGPVGGKARPEAAEAPEGVDPPRRHHR------
                                                                                                                          88 WRAWMOKSHKTRNOVGKLGE-----ACVGGKGAEEERDPGEQ------PPQHRTL 131
                                                                                                                                                                                                            30 PTAASTPRSERPGPGGGVCEPRGGEPSSG--PVRRELKQFLGWLKKHAYCSNLSFRLYDQ 87
                                                                                -HRDKDKTPAAGDQDRAEAPKAESGEPGAREERPRADRSHSKEAAGPPEARTS 905
                                                                                                                                                                                                                                                                                                                                                                                            protein '
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22.0%; Pred. No. 52;
ative 13; Mismatches
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Search completed: September 16, 1999, 20:41:08 Job time: 5437 sec

Scoring table:

Title: Perfect score:

Run

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OM protein

Sequence:

synapsin Ib - huma prolactin receptor synapsin Ia - bovi synapsin Ib - bovi

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d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
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Copyright (c) 1993 - 1998 Compugen
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C; Accession: A49364
R; Shaw, D.J.; McCurrach, M.; Rundle, S.A.; Harley, H.G.; Crow, S.R.; Sohn, K.; Inlied Genomics 18; 673-679, 1993
A; Title: Genomic organization and transcriptional units at the myotonic dystrophy local parameter number: A49364; MUID:94140369
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                                                                                                                                                                                                                                                                                                                                   RESULT
A49364
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                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-553 <SHA>
A;Cross-references: GB:L19267; NID:g306711; PID:g306712
                                                                                                                                                                                            A;Reference number: A49364;
A;Accession: A49364
A;Status: preliminary
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A; Residues: 1-416 <TAN>
A; Cross-references: EMBL:D11117; NID:g219879; PID:d1002368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Taniguchi, Y.; Fujii, A.; Moriuchi, T.
Biochim. Biophys. Acta 1132, 332-334, 1992
A; Title: Cloning and sequencing of the human
A; Reference number: S27198; MUID: 93041940
A; Accession: S27198
                                                                                                                                                                                                                                                                                                                     59 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Homo sapiens (man)
C; Date: 13-Jan-1995 #sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N; Alternate
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A;Introns: 165/1
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Best Local Similarity

Matches 34; Conserv
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Best Local S
Matches 31
                                                                                                                                                                                                                                                                                   ;Species: Homo sapiens (man)
;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: homeotic protein Hox B3; homeobox homology Keywords: DNA binding; homeobox; nucleus; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession:
                               349
                                                                                                                                                                                                                                                                                                                                                                                          148 MKE----
74 HAYCSNLSFRLYDQWRAWMQKSHKTRNQVGKLGEACVGGKGAEEERDPGEQPPQHRTLLS
                                                          30
                                                                                                                                                                                                                                                                                                                                                                                                    71 LKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQVGKLGEACVGGKGAEEERDPGEQPPQHRT: |: | |: || : || : ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
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N
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                                                    PTAASTPRSERPGPG------GGVCEPRGGEPSSGP-VRRE-----LKQFLGWLKK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                          GSQPPGLNSEQQPPQPPPPPPTLPPCSPTNPGGGVPAKKPKGGPNASSSSATISKQIFPW 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSKKAGIWSEWSHPTAASTPRSERP----GPGGGV--CEPRGGEPSSGPVRRELKQFLGW 70
                           PPAASSSRGGEPGPGPLPRSLSRSNSLPHPAGGGKAGGPGVAAEPGTPFSIGRF----- 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 25.8
31; Conservative
                                                                                  Conservative
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    human (fragment)

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                                                                                               10.7%;
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705
581
706
670
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                                                                                                                                                                                                                                                                                                                                                                                     -----SRQNSKQKNSCATAGESC-----EDKSPPGPASKRVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein Hox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                               Score 92.5; DB
Pred. No. 0.21;
17; Mismatches
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A35363
B35363
I45971
E30411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 94; DB 2
Pred. No. 0.11;
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                                                                                                            DB
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                                                                                 48;
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                                                                                                           Length 553;
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regulation

Gaps

Q \$ 450-64.16

PID:g219880

Result

Score

73.5 73.5 72.5 72.5 72.5 72.5

70.5

Gaps

9

74.5 74

77.5 77

82.5 80.5

76.5

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                                                                                                                                                                                                                                                                                                                   finger protein MZF1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N; Alternate names: 64K polyadenylylation
                                                                                                               ;Status: preliminary
;Molecule type: mRNA
;Residues: 1-485 <HRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Map position: 21q22.3-21q22.3
Superfamily: unassigned ribonucleoprotein repeat-containing
Keywords: heterotrimer; phosphoprotein; RNA binding
;17-84/Domain: ribonucleoprotein repeat homology <RRMI>
                                                          Gene: GDB:ZNF42; MZF-1
                                                                                                                                                                                      Reference number:
                                         Cross-references:
                                                                                              Cross-references:
                                                                                                                                                                                                                                                          Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 24-Sep-1998 Accession: A40751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GB:M85085; NID:g181138; PID:g181139
Note: sequence extracted from NCBI backbone (NCBIN:82408, NCBIP:82414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takagaki, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eavage stimulation factor 64K chain -
                                                                                                                                                                                  Hromas, R.; Collins, S.J.; Hickstein, D.; Raskind, W.; Deaven, L.L.; O'Hara, Biol. Chem. 266, 14183-14187, 1991
Title: A retinoic acid-responsive human zinc finger gene, MZF-1, preferentia. Reference number: A40751; MUID:91317761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene: GDB:CSTF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
Residues: 1-577 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: A40220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takagaki, Y.; MacDonald, C.C.; Shenk, T.; Manley, J.L. oc. Natl. Acad. Sci. U.S.A. 89, 1403-1407, 1992
Title: The human 64-kDa polyadenylylation factor contains
Reference number: A40220; MUID:92159058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species:
                                                                                                                                                                   Accession: A40751
                                                                                                                                                                                                                                                                                                                                                                                                            352
                                                                                                                                                                                                                                                                                                                                                                                                                                            123 EQPPOHRTLISKHRTRGSCPRADGVRREVRG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 SKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGEPSSGPVRRELKQFLGWLKKHAYC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
                                                                                                                                                                                                                                                                                                                                                                                                          QGPPMHH--VPGHESRGPPP-----HELRG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNLSFRLYDQWRAWMQKSHKTRN---QVGKLGEA-----CVGGKGAEEER----DPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMQGGVPAPGQMPAAVTGPGPGSLAPGGGM-QAQVGMPGSGPVSMERGQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VPMQDP-RAAMQRGSLPANVPTPRGLLGDAPNDPRGGTLLSVTGEVEPRGYLGPPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KHRTRGS--CPR 143
                                                                                                                                                                                                                                                                                                  Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5-residue repeats
                                       GDB:125898; OMIM:194550
                                                                                            GB:M58297; NID:g189043;
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     transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 84; DB
Pred. No. 1.4;
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                                                                                            PID:g189044
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   zinc
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                                                                                                                                                                                                 gene, MZF-1, preferentially expres
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   finger
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                                  A; Molecule type: DNA
A; Residues: 1-816 < VAN>
                                                                                                                                                                                         N; Alternate names: hypothetical
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                                                                    A; Reference number: A; Accession: S64439
                                                                                                          submitted to the Protein
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A; Experimental source:
                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Fukumor1, F.;
                                                                                                                           Van Dyck, L.
                                                                                                                                          Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: A251
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lulase (EC 3.2.1.4) 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                             398 EPLGDAPPSEPSDPPPPSEPEPDPGEPDP
                                                                                                                                                                                                                                                                                                                                             104 -KLGEACVGGKG----AEEERDPGEQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 WSEWS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76
                                                                                                                                              S64439
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EMBL: 272915; NID: g1323214;
e: strain S288C
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                                                                                                          Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.5%;
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                                                                                                                             de Wergifosse,
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A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages in A;Pathway: cellulose degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M14781; GB:X53449; NID:g142659; A;Experimental source: strain N-4, plasmid pNK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Title: Nucleotide sequences of two cellulase genes;Reference number: A91825; MUID:87056924
                                                     Species: Saccharomyces cerevisiae
Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 14-Nov-1997
                                                                                                                                                                                                                                                                                                                              340 -DPDPGEPDPTP-PSDPGEYPAWDPNQIYTNEIVYHNGQLWQAKWWTQNQEPGANQYGPW 397
                                                                                                                                                                                                                                                                                                                                                                                                                     283 WANWSLTHKDESSAALMPGANPTGGWTAAELSPSGAFVREKIRESASIPPSDPTPPS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 VHTGEQPFRCAECGQSFRQRSNLLQHQRIHGDPP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 GVGPALITTRWRSPRGRS---RGRPSTGGGVV--RGGRCDVCGKVFSQRSNLLRHQKIHT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 GSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE-PSSGPVRRELKQFLGWLKKHA 75
                                                                                                                                                                                                                                                                                                                                                                          CEPRGGEPSSGPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRA--WMQKSHKTRNQVG-- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----YCSNLSFRLYDQWRAWMQKSHKTRNQV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endo-1,4-beta-glucanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POHRTLLSKHRTRGSCP
                                                                                                       yeast (Saccharomyces cerevisiae)
1 protein G6382
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 82.5;
Pred. No. 1
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                                                                                                                                                                                                                                                                                       126
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P.; Purnelle,
e, May 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 488;
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                  B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                  Talla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-D-glucans
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PID:e243523;

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MIFS: YGR13

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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Run on: OM protein - protein search, using sw model

September 17, 1999, 03:10:12; Search time 35.09 Seconds (without alignments) 124.867 Million cell updates/sec

Title: Perfect score: Sequence: US-09-037-657-17 864

GTVYFVQVRCNPFGIYGSKK.....RTRGSCPRADGVRREVRGSG 155

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database : SwissProt_37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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h 10.9%; Score 94; DB 1; Length 416; Similarity 25.8%; Pred. No. 0.09; 31; Conservative 16; Mismatches 43; Indels

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-!- DISEASE: MAY HAVE A ROLE IN THE DEVELOPMENT OF MENTAL SYMPTOM SEVERE CASES OF MYOTONIC DYSTROPHY.
-!- SIMILARITY: TO S.POMBE SPACIZB10.03 AND TO C.ELEGANS C08B6.7.
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NEVILLE C.E., WORMSKAMP N., SEGERS B., BA
DE JONG P.J., WIERINGA B., KORNELUK R.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CST2_HUMAN
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PTM: KNOWN TO BE PHOSPHORYLATED.
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RNP).
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ONE OF THE MULTIPLE FACTORS REQUIRED CLEAVAGE OF MAMMALIAN PRE-MRNAS. THI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preferentially expressed in myeloid cells., , BIOL. CHEM. 266:14183-14187(1991).
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EUKARYOTA; METAGOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A retinoic acid-responsive human zinc finger gene, MZF-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. SEDLINE; 91317761.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -DEC-1992 (REL. 24, CREATED)
-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYELOID CELLS.
INDUCTION: BY RETINOIC ACID.
SIMILARITY: BELONGS TO THE KRUEPPEL SUBFAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN DIFFERENTIATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEMOPOIETIC DEVELOPMENT. SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: MAY BE ONE REGULATOR OF TRANSCRIPTIONAL EVENTS DURING
                                                                                                                                                                                                                                                                                                                                                                                                                              194550;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGPPMHH--VPGHESRGPPP----HELRG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VPMQDP-RAAMQRGSLPANVPTPRGLLGDAPNDPRGGTLLSVTGEVEPRGYLGPPH 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNLSFRLYDQWRAWMQKSHKTRN----QVGKLGEA-----CVGGKGAEEER----DPG
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                                                                                                                                                                                                                                                                                                                                                                             PF00096; zf-C2H2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQPPQHRTLLSKHRTRGSCPRADGVRREVRG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMQGGVPAPGQMPAAVTGPGPGSLAPGGGM-QAQVGMPGSGPVSMERGQ-
                                                                                                                                                                                                                                                                                                                                                                                                PS00028; ZINC_FINGER_C2H2;
                                                  107
135
191
191
236
292
3202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MYELOID ZINC FINGER 1) (MZF-1).
                                                                                                                                                                                                                                                                                                       ZINC-FINGER; DNA-BINDING; NUCLEAR PROTEIN
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                             C2H2-TYPE.
                                                                                                                                                                                                                                                GLY/PRO-RICH
                                                                                                                                                                                                                                                             SP/GLU-RICH (ACIDIC).
C2H2-TYPE ZINC-FINGERS.
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                                                                                                                                                                                                                  C2H2-TYPE ZINC-FINGERS
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24 WSEWS----

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                    Query Match
Best Local :
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                                                                                CELLULOSE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZN_FING
ZN_FING
ZN_FING
SEQUENCE
                                                                                                                                                          PIR; A25156; A25156.
PROSITE; PS00659; GI
                                                                                                                                                                                     EMBL; M14781; G142660; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACILLUS SP. (STRAIN N-4).
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAB;
                                                                                                                                                                                                                                                                                                                                                       TOKUMORI F., SASHHARA N., KUDO T., HORIKOSHI K.;

"Nucleotide sequences of two cellulase genes from alkalophilic actions sp. strain N-4 and their strong homology.";

J. BACTERIOL. 168:479-485(1986).

-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC LINKAGES IN CELLULOSE.

-1- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
ENDOGLUCANASE A (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE) (CELLULASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P06566;
                                                                                                                                               FAM; PFOO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÆDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 -DPGEQP------PQHRTLLSKHRTRGSCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE PNK1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 GERPFYCSECG-----RSFSRSSHLLRHQLTHTEERPFYCGDCGQGFYRSARLEEHRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 VHTGEQPFRCAECGQSFRQRSNLLQHQRIHGDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 ----YCSNLSFRLYDQWRAWMQKSHKTRNQV------GKLGEACVGGKGAEEER- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 GSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPRGGE-PSSGPVRRELKQFLGWLKKHA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 GYGPALITTRWRSPRGRS---RGRPSTGGGVV--RGGRCDVCGKVFSQRSNLLRHQKIHT 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
                    Similarity
                                                        O150; cellulase; 1.

O150; cellulase; 1.

DEGRADATION; HYDROLASE; GLYCOSIDASE.

163 163 PROTON DONOR (BY SIMILARITY).

252 252 NUCLEOPHILE (BY SIMILARITY).

252 253 NUCLEOPHILE (CRC32;
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485
    Conservative
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                                                                                                                                                       GLYCOSYL_HYDROL_F5; 1.
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   14;
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                   Score 82.5;
Pred. No. 1
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Pred. No. 1.1;
8; Mismatches
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908B33F1 CRC32;
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                              Length 488;
   Indels
 51;
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RESULT 7
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Best Local (
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                01-OCT-1996
01-OCT-1996
                                                          YG3A_YEAST
P53278;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not rementities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U71293; G1772656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Thyroid hormone-responsive genes in develops novel synaptotagmin and a hairless homolog."
J. NEUROSCI. 16:7832-7840(1996).
- IF FUNCTION: MAY ACT AS A TRANSCRIPTION FACT
                                                                                                                                                                                                                                                                                                                                                                                                                                  METAL-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                              ZINC-FINGER; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
RODENTIA; SCIUROGNATHI; MURIDJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAIRLESS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5-JUL-1998 (REL.
L5-JUL-1998 (REL.
L5-JUL-1998 (REL.
                                                                                                                                                  375
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                                                                                                                                                                                                                                    LKKHAYCSNLSFRLYDOWRAWMOKSHKTRNOVGKLGEACVGGKGAEEERDPGEO--PPOH 128
                                                                                                                                              HTKLKKTWLTRHSEQFECPGGCPGKGESPATGLRALKRAGSPEVQGA
                                                                                                                                                                                                                                                                                                  WSHPTAAS----
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                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                           RTLLSKHRTRGSCP------RADGVRR-----EVRGS 154
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1181 AA;
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    (REL.
(REL.
(REL.
2 92.7
                                                                                                                                                                                                                                                                                                                              Conservative .
                                                                           STANDARD;
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34, CREATED)
34, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
KD PROTEIN IN ASN2-PHB1 INTERGENIC
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36, LAST SEQUENCE UI
36, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                  619
                                                                                                                                                                                                                                                                                              --- TPRSERPG---PGGGVCE----PRGGEPSSGPVRRELKQFLGW 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR PROTEIN;
                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                          Score 81; DB
Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERTEBRATA;
AE; MURINAE;
                                                                           PRT;
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RATTUS.
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 REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                               REGULATION;
                                                                                                                                                                                                                                                                                                                           78;
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RIFTIIDAE;
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01-JUL-1993 (REL. 26, LAST SEQUENCE
15-JUL-1998 (REL. 36, LAST ANNOTATIO
FIBRIL-FORMING COLLAGEN ALPHA CHAIN
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P30754;
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                                                                                                                                                                                                                                                                                                                                                "Amino-acid sequence an collagen from the tube
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MANN K., GAILL F.,
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SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
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SACCHAROMYCETACEAE;
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EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
                                        EXTRACELLULAR MATRIX; CONNECTIVE TISSUE;
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                                                              I- SUBUNIT: HOMOTETRAMER.
I- PTM: ALL THE "X" ARE PROBABLY GLYCOSYLATED HYDROXYLYSINES
IR; S22915; S22915.
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                                                                                                     worms collected at deep sea hydrothermal wor. BIOL. 221:209-223(1991).
FUNCTION: FIBRIL-FORMING COLLAGEN.
SUBUNIT: HOMOTETDANDER.
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                                                                                                                                                                                                        WIEDEMANN H.,
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DEL BINO S.,
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205
COLLAGEN.
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AC 000975;

AC 000975;

DT 01-OCT-1996 (REL. 34, CREATED)

DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-CONOTOXIN-SENSITIVE N-

DE TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT).

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GN CACNELIAS

OS HOMO SAPIENS (HUMAN).
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TRANSMEM
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SUBMITTED (FEB-1997) TO EMBL/GENBANK, DDBJ DATA BANKS.
SUBMITTED (FEB-1997) TO EMBL/GENBANK, DDBJ DATA BANKS.
-I- FUNCTION: HIGH VOLTAGE-ACTIVATED CALCIUM CHANNEL SENSITIVE CALCIUM CHANGEL SENSITIVE CALCIUM CHEGA-CONOTOXIN. MAY MEDIATE THE OMEGA-CONOTOXIN-SENSITIVE CALCIUM INFLUX REQUIRED FOR NEUROTRANSMITTER RELEASE AT MANY SYMAPSES. MAY ALSO PLAY A ROLE IN DIRECTED MIGRATION OF IMMATURE NEURONS.
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-I- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM.
-I- ALTERNATIVE PRODUCTS: TWO FORMS OF ALPHA-1B (ALPHA-1B-1 AND ALPHA-1B-2) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THAT OF ALPHA-1B-1.
-I- SIMILARITY: TO OTHER CALCIUM CHANNEL ALPHA SUBUNITS.
                                                                                                                                                                                                                                               TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                  EMBL; M94172; G179758; -. EMBL; M94173; G179760; -. EMBL; U76666; G1809331; -. MIM; 601012; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METASOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
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TISSUE-BRAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage
                                                                                                                                                                                                                                                                                                                                              VOLTAGE-GATED CHANNEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     its content
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RAL_CHITE BARL_CHITE BARL_CHITE BARL_CHITE BARL_CHITE BARL_CHITE BARL_CHITE BARL_CHITE DARLAGY 21-UUL-1986 (REL. 01, CARATED) 21-UUL-1986 (REL. 01, LAST SEQUENCE UPDATE) BALBIANI RING PROTEIN 1 (GIANT SECRETORY PROTEIN I-A) (GSP-IA) ERRICAGORY CHIRONOMUS TENTANS (MIDGE). EUKARYOTA; METALOA; ARTHOPODDA; TRACHEATA; HEXAPODA; INSECTA; PTERYGOTA; DIPTERA, NEMATOCERA; CHIRONOMOIDEA; CHIRONOMIDAE; [1] NOUNCE OF 1-116 FROM N.A. (CLONE PCTBR1-1). TISSUE-SALIVARY GLAND; MEDLINE: 93238361. CASE S.T., BYERS M.R.; "Repeated nuclectide sequence arrays in Balbiani ring 1 of Chironomus tentans contain internally noorepeating and subrepeating elements."; [2] CASE S.T., BYERS M.R., (CLONE PCTBR1-1). TISSUE-SALIVARY GLAND; MEDLINE: 93238361. CASE S.T., SUMEGI J., DANHEDLT B.; "FYIGHORE FOR 7-174 FROM N.A. (CLONE PCT21). SEQUENCE OF 7-174 FROM N.A. (CLONE PCT21). "TISSUE-SALIVARY GLAND; "TISSUE-SALIVARY GLAND; THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR THIS SHIEST FROM THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR THIS SHIEST FROM THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR THE SHIEST FROM THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR THE SHIEST FROM THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR THE SHIEST FROM THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR THE SHIEST FROM THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR THE SHIEST FROM THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR THE SHIEST FROM THE S	Query.Match 9.0%; Score 78; DB 1; Length 2339; Best Local Similarity 23.2%; pred. No. 17; Matches 33; Conservative 15; Mismatches 38; Indels 55; Gaps 8; 28 SHPTAASTPRSERPGPGGGVCEPRGGEPSGPVRRELKQFLGWLKKHAYCSNLS 81	CARBOHYD 751 751 CARBOHYD 1063 1063 POTENTIAL. CARBOHYD 1563 1563 POTENTIAL. CARBOHYD 1563 1563 POTENTIAL. CARBOHYD 1675 1867 CARBOHYD 2169 2169 CARBOHYD 2169 2169 CARBOHYD 2207 2207 CARBOHYD 2207 2207 CARBOHYD 2169 POTENTIAL. CARBOHYD 2169 POTEN

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                          CELL 81:1043-1051(1995).

-!- FUNCTION: INVOLVED IN CARYOGAMY (NUCLEAR FUSION), A PROCESS REQUIRED FOR SEXUAL SPORULATION.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.

-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                                                                                                                                                                                                                          PODOSPORA ANSERINA.

EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
SORDARIALES; SORDARIACEAE; PODOSPORA.
                                                                                                                                    discovered as a
                                                                                                                                                 PANVIER-ADOUTTE A., SIMONET "A nonmammalian homolog of t
                                                                                                                                                                          BERTEAUX-LECELLIER V., PICARD M., THOMSON-COFFE C., ZICKLER D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                   EDLINE; 95323960
                                                                                                                                                                                                                                                                                                                                      )1-OCT-1996 (REL. 34, CREATED)
11-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
11-NOV-1997 (REL. 35, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; K00447; G156531;
EMBL; J01055; G552075;
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nes 37; Conserv
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    SWISS-PROT entry is copyright.
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                                                                                                                                 homolog of the PAF1 gene (Zellweger syndrome) gene involved in caryogamy in the fungus Podo
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PROTEIN CAR1 (PEROXIN-2).
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23.9%; Pred. No. 1.3;
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It is produced through a collaboration
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CLONE
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Best Local :
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EMBL; X14112; G59536;
EMBL; X14112; E312351;
PIR; I30085; WMBEH6.
                                                       wise by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the En
                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                 herpes simplex virus type 1.";
J. GEN. VIROL. 69:1531-1574(1988).
-!- EUNCTION: TEGUMENT PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                         MCGEOCH D.J., DALRYMPLE M.A., MCNAB D., PERRY L.J., SCOTT J
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 88274327.
                                                                                                                                                                                                                                     MCGEOCH D.J., DALRYMPLE M.A., DAVISON A.J.; DOLAN A., FRAME M.C., MCGRAB D., PERRY L.J., SCOTT J.E., TAYLOR P.;
"The complete DNA sequence of the long unique region in the genom
                                                                                                                                                                                                                                                                                                                                 VIRUSES; DSDNA VIRU
ALPHAHERPESVIRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                               HERPES SIMPLEX VIRUS (TYPE 1 / VIRUSES; DSDNA VIRUSES, NO RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Similarity 21.48;
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                                                                                                                                                                                                                                                                                                                                                                                                        10, CREATED)
10, LAST SEQUENCE UPDATE)
25, LAST ANNOTATION UPDATE
                                                                                                                                                                                                                                                                                                                                SIMPLEXVIRUS
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NA STAGE; HERPESVIRIDAE;
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7FB46748 CRC32;
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ASP/GLU-RICH (HIGHLY ACIDIC).
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-i- SIMILARITY: BELONGS TO CELLULASE FAMILY E (FAMILY 9 OF G.
                PROSITE; PS00018; EF HAND; UNKNOWN_1, PROSITE; PS00448; CLOS_CELLULOSOME_RPT; PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2;
                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ev
                                                                                                                                                                                                   -1- SIMILARITY: CONTAINS 1 CELLULOSE-BINDING DOMAIN (CBD)
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-I- FUNCTION: THE BIOLOGICA
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01-FEB-1995 (REL.
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P37700;
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                                                                                                                                                                                                                                                                                                                                         FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENSYMES;
(1) ENNOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
(2) EXOCELLOBIOHYDROLASES THAT CUT THE DISSACCHARIDE CELLOBIOSE FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
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PATHWAY: CELLULOSE DEGRADATION.
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                                                                                                                                                                                                                                                                                                                   BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
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MATHUR M. KOLATUKUDY P.E.;

"Molecular cloning and sequencing of the gene for mycocerosic acid
synthase, a novel fatty acid elongating multifunctional enzyme, fro
synthase, a novel fatty acid elongating multifunctional enzyme, fro
synthase, a novel fatty acid elongating multifunctional enzyme, fro
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                                                                                                                                                                                                                                                                            MEDLINE;
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FUNCTION: CATALYZES THE ELONGATION OF N-FATTY METHYLAMALONYL-COA (NOT MALONYL-COA) AS THE ELFORM MYCOCEROSYL LIPIDS.
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                                                                                                                      SIMILARITY: PARTIAL TO S.ERYTHRAEA ERYTHRONOLIDE 4, AND TO VERTEBRATE FATTY ACID SYNTHASES.
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EMBL; M95808; G149980; PIR; B44110; B44110.

PHOSPHOPANTETHEINE;

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EMBL; L34783; G903847; -.
PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
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                                                                                                                use by non-profit institutions as a modified and this statement is not remember a license agreement.
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                                                                                              or send an email to license@isb-sib.ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              )REOCHROMIS NILOTICUS (NILE TILAPIA) (TILAPIA NILOTICA).
SUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
FELEOSTEI; EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA; PERCIFORMES;
ABROIDEI; CICHLIDAE; TILAPIA.
                                                                                                                                                                                                                              his SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                 ANDRA O., SOHM F., DE LUZE A., PRUNET P., EDERY M., KELLY P.A.;
Expression cloning of a cDNA encoding a fish prolactin receptor.";
ROC. NATL. ACAD. SCI. U.S.A. 92:6037-6041(1995).
I- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDLINE; 95320210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NOV-1997
                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVAVSSFGMSGTNVHAIVEE--APAEASAPES---SPGDAEVGPRLFMLSSTSSDALRQT 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKQFLGWLKKHAYC---SNLSFRL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGVCEPR---GGEPSSGPVRRE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REL. 35, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOSYNTHESIS; MULTIFUNCTIONAL ENZYME; PHOSPHOPANTETHEINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REL. 35, REL. 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DROLASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         etoacyl-synt; ]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BETA-KETOACYL REDUCTASE.
ACYL CARRIER (ACP).
BETA-KETOACYL SYNTHASE (BY SIMILARITY).
ACYL TRANSFERASES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHOPANTETHEINE (BY SIMILARITY)
W; E1406CB6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BETA-KETOACYL SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADP (KR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACYL TRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                 It is produced through a collaboration informatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REDUCTASE
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                                                                                                                                                                                 There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                           as its content
                                                                                                                                         Usage
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Best Local S
Matches 14
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SEQUENCE
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200 GGTYLIQVRCKP-----DHGFWSEWSSTSYVKVP 228
                                                                                                                                                                        DOMAIN
                                                                                                                                                                                   DOMAIN
                   1 GTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 36
                                                14;
                                                          Similarity
                                               Conservative
                                                                                                       101 PO' 70810 MW;
                                                           38.9%;
                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
                                                          Score 72.5;
Pred. No. 14;
                                                                                                                                                                   FIBRONECTIN TYPE-III.
                                                                                                                                                                              CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                PROLACTIN RECEPTOR
                                                                                                         E9A4E553 CRC32
                                            Mismatches
                                                                                                                                                                                                                                                   SIGNAL; REPEAT
                                                                   DB 1;
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Search completed: September 17, 1999, 03:10:13 Job time: 293 sec

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atabase :
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                                                                                                                                                                                                                                            75.
7
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Match
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864
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138.330 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.
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sp_unclassified:*
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Q19204
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                                                                                                                                                                                                                                                                                                                                                                                                            075462 homo sapien
002661 bos taurus
095873 homo sapien
064807 arabidopsis
                                                              P96291 mycobacteri
Q92529 homo sapien
O93404 oreochromis
                                                                                                                                                                                                                                                                                                   Q9zbf5 streptomyce 080394 mesembryant
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042798 schizosacch
                                                                                                                                                                                 075154 homo sapien
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Q97641 equus cabal
                                                                                                                                                                                                                                                                                                                                                              083470 treponema p
Q19204 caenorhabdi
064428 chlorella v
                                                                                                                                                                                                                                  Q90711 gallus gall
Q44128 acetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                   Q69088 human herpe
                                                                                                                                                                 070204 mus musculu
                                                                                                                                                                                                  080770 arabidopsis
081009 arabidopsis
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P70336 mus musculu
homo sapien
homo sapien
homo sapien
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OCCOSE DATES	RESERVED TO SOLUTION OF THE SO	
1 GTYYFYOYRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERP 1	SULT 1 5462 PRELIMINARY; PRT; 422 AA. 075462; PRELIMINARY; PRT; 422 AA. 075462 01-NOV-1998 (TIEMBLITEL 08, Created) 01-NOV-1998 (TIEMBLITEL 10, Last sequence update) 01-MAY-1999 (TIEMBLITEL 10, Last sequence update) 01-MAY-1996 (TIEMBLITEL 10, Last sequence update) 1	30 72 8.3 670 11 088935 088935 mus musculv 31 72 8.3 1537 13 092072 9311us gall 32 71.5 8.3 457 4 013518 33 71.5 8.3 1208 0924761 013518 homo sapien 34 71.5 8.3 140 5 025212 025212 100001a color 35 71.5 8.3 207 5 076587 076587 076587 caenorhabdi 37 71.5 8.3 296 12 093645 093645 caenorhabdi 38 71 8.2 629 2 025217 025212 100001a color 39 71 8.2 629 2 025217 025212 100001a color 40 71 8.2 1804 1 02548 076587 093645 caenorhabdi 41 70.5 8.2 1804 1 02548 076587 092617 streptomyce 42 70.5 8.2 1804 1 015468 076587 060247 homo sapien 44 70.5 8.2 819 4 013443 013443 homo sapien 45 70.5 8.2 411 12 081813 081813 hepatitis c
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Matches 20
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Best Local (
                                                      01-AUG-1998 (TIEMBLIEL 07, Created)
01-AUG-1998 (TIEMBLIEL 07, Last sequence update)
01-MAY-1999 (TIEMBLIEL 10, Last annotation update)
01-MAY-1999 (TIEMBLIEL 10, Last annotation update)
PUTATIVE SERINE CARBOXYPEPTIDASE I.
F21P24.3 OR T20K9.18.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; endicotyledons;
core endicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
NON_TER
SEQUENCE
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01-MAY-1999
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      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF129756; AAD18083.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABBASI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutherla;
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PFAM; PF00090; tsp_1; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASKY S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-SUBCOMMISSURAL ORGAN;
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SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                  WDHVDSGGT---RRPGVSPEGGLSVPGPGAPLEKPGRRE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
20; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FEB-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JUL-1996) to the 561; CAA69868.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DICKHOFF
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425 AA;
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                                                                                                                                                                                                                                                                   PRELIMINARY;
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    N.A
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43721 MW;
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LORETZ C., MADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,5,5
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Pred. No. 0.85
4; Mismatches
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                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B0E58CB3 CRC32;
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IN A., DORS
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-FVQVRCNPEGIYGSKKAGIWSEWSHPTAA--STPRSERPGPGGGVCEPR--GG

Query Match Best Local S Matches 33

l Similarity 33; Conserv

9.0%; llarity 32.0%; Conservative

9

Score 78; DB Pred. No. 2.6; 9; Mismatches

2; 39;

Indels

Gaps 53

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Best Loc
Matches
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                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.

DODSON R., GWINN M., HICKEY E.K., CLAYFON R., KEFCHUM K.A.,

SODERGREEN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON

KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBAC

MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARI

MCDONALD L., ARTIACH P., BOWMAN C., WATTHEY L., WEIDMAN J., SMITH F
Submitted (MAR-1998) to the EMBL; AE001222; AAC65441.1; SEQUENCE 593 AA; 65567 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROUNSIEY S.D., LIN X., KETCHUM K.A., CROSBY M. SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.F. SOMERVILLE C.R., VENTER J.C., "Arabidopsis thaliana chromosome II BAC T20K9 Submitted (AUG-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                       MEDLINE; 98332770.

FRASER C.M., WORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A., DODSON R., GWINN M., MCLEOD M.P., SALZBERG S., PETER KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTE KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTE MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C.,
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01-NOV-1998 (TremBLrel.
01-NOV-1998 (TremBLrel.
CONSERVED HYPOTHETICAL E
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SEQUENCE 433 AJ
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                                                                                                                                                                                                                                                                                                                                                          Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                      cience
                                                                                                                                                                                               Complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC004401; AAC17814.1; ... AC004786; AAC32443.1; ... PF00450; serine_carbpept;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
19; Conserv
                                                                                                                                                                      281:375-388(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49233 MW;
                                                                                                                                                                                                                           ROBERTS K.,
                          to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.2%;
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Last sequence Last anno
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Pred. No. 1.3;
9; Mismatches
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16898991 CRC32;
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                                                      SMITH H.O.
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Query Match
Best Local 9
064428;
01-AUG-1998
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EMBL; U29378; AAA68721.1; -.
PFAM; PF0090; tsp_1; 6.
SEQUENCE 957 AA; 106808 MW; 03F05B40 CRC32;
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                                                                                                                                                                                                                                                                                 608 GTWSLWTSCTATC------GGGYRKRNRACSITG---
                                                                                                                                                                                                               646 VCSSESCPSVLRVGNEWSTWTEWNH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A RAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., ARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., ONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., IGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., MARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ukaryota; Metazoa; Nemato
habditina; Rhabditoidea;
                                                                                                                                                                                                                                         76 YCSNIS----FRLYDOWRAWWOKSHKTRNOVGKLGEACVGGKGAEEERDPGEQPPQHRTL 131
                                                                                                                                                                                                                                                                                                                     22 GIWSEWSHPTAASTPRSERPGPGGG-----VCEPRGGEPSSGPVRRELKQFLGWLKKHA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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2.2 Mb of contiguous
legans.";
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                                                                                                                                   LSPHRTLAFDCPGENKVTNELR
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(TrEMBLrel. 07,
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                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                   9.0%;
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oldea; Rhabditidae; Peloderinae; Caenorhabditis.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   Score 78; I
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                                       PRT; 1309
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                                     B
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Best Local S
Matches 20
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Matches 36
         1127
                                                                                                                                    PROSITE;
                                                                                                                                                           J. Biol. Chem. 270:29051-29054()
EMBL; U38481; AAB37540.1;
PFAM; PF00130; DAG_PE-bind; 1.
PFAM; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                      MEDLINE; 9
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01-MAY-1999
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                             Eukaryota;
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01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                    hich translocates the kinase
                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
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HIGASHIYAMA T., NOU
"Zepp, a LINE-11ke
                                 42 GPGGGVCEPRGGEPSSG---
                                                                                                                                                                                                                                       A novel serine/threonine
                                                                                                                                                                                                                                                                                                                utheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 QHRTLLSKHRTRGSCPRADGVRREVRGSG
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GSGPGDAEPDDGFPESRLEGWLSLPVRNNTKKF-GWVKKYVIVSSKKILFYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGWLKKHAYCSNLSFRLYDOWRAWMOKSHKTRNOVGKLGEACVGGKGAEEERDPG-EOPP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSKKAGIWSEWSHPTAASTPRSERP-----GPGGGVCEPRGGEPSSGPV----RRELKQF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB008896; BAA25763.1; -. PF00078; rvt; 1.
                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Conserv
                                                                                                                                                                                                                                                                                                         Metazoa; Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                    MANSER E., TAN L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ARCRARPGASGSDGARARAHPSG 1083
                                                                                                                                    1379 AA;
                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                     ER E. TAN L., LIM L.;

E/threonine kinase binding the

ates the kinase to peripheral n

270:29051-29054(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymerase.
NA; 141659 MW; C874E321 CRC32;
                                                                                                                             PROTEIN_KINASE_ST; 1.
159434 MW; 9BCEBCFC CRC32;
                                                                        9.0%;
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                                                         Score 78; DB 1
Pred. No. 6.4;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 78;
Pred. No.
                           PVRRELKQFLGWLKKHAYCSNLSFRLYD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155
                                                                                      DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                            ₹
                                                                                                                                                                                                                    e Ras-related membranes.";
                                                          20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -CLGGLG----QAWPGQDQPP 1060
                                                                                    Length 1379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1309;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                         Rattus
                                                                                                                                                                                                                                RhoA GTPase
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RESULT P70336

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Best Loc
Matches
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01-MAY-1999
01-MAY-1999
01-MAY-1999
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1997 (TremBLrel. 02, Created 01-FEB-1997 (TremBLrel. 02, Last se 01-MAY-1999 (TremBLrel. 10), Last at RHO-ASSOCIATED COILED-COIL FORMING (RHO-ASSOCIATED, COILED-COIL FORMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P70336;
                                  *RINASHI H., HOPWOOD D.A.;

"A set of ordered cosmids and a detailed the 8 mb Streptomyces coelicolor A3(2) che Mol. Microbiol. 21:77-96(1996).

EMBL; AL035206; CAA22767.1; ...
                                                                                                                                                                                                                                                                                                             STRAIN-A3(2);
SEEGER K.J., HARRIS !
Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9ZBF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                       STRAIN=A3(2);
BENTLEY S.D., PARKHILL J., F
Submitted (JAN-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, C:
01-MAY-1999 (TrEMBLrel. 10, L:
01-MAY-1999 (TrEMBLrel. 10, L:
HYPOTHETICAL 32.4 KD PROTEIN.
Hypothetical
SEQUENCE 2
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales; Streptomycineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SC9B5.25.
                                                                                                                                    REDENBACH M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corming
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                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           EQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPGGGVCEPRGGEPSSG-----PVRRELKQFLGWLKKHAYCSNLSFRLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00130; DAG_PE-bind; 1.
PF00069; pkinase; 1.
TE; PS00108; PROTEIN_KINASE_
NCE 1388 AA; 160584 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein serine/threonine
tt. 392:189-193(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Mouse)
Hetazoa; Chordata; Craniata; Vei
Hetazoa; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                  KIESER H.M.,
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  32399 MW;
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                                                                                                                                                                                                                BARRELL B.G., RAJAN
e EMBL/GenBank/DDBJ
                                                                                                                                    DENAPAITE
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Pred.
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t annotation update
ING KINAGE 2
61D7FCEE
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FCB26B88 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                             Streptomycetaceae;
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                                                                       ed genetic and chromosome.";
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ae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               멂
CRC32;
                                                                                                                                                                                                                RAJANDREAM M.A.;
/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
                                                                                                                                  EICHNER
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Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coiled-coil
                                                                                           physical
                                                                                                                                    COLLOM
                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces.
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Query Match Best Local S

Similarity

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Score Pred.

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Length

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Best Local
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SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
LIN X., KAUL S., SHEA T.P., F
BARNSTEAD M.E., MASON T.M., B
CARRERA A.J., CREASY T.H., BU
FRASER C.M., VENTER J.C.;
                                                                                                                                                                 0920C7
0920C7;
01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 080394;
01-NOV-1998
01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TIEMBLIEL 08, 01-NOV-1998 (TIEMBLIEL 08, 01-NOV-1998 (TIEMBLIEL 08, TRANSCRIPTION FACTOR VP1.
                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesembryanthemum crystallinum (Common ice plant).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopeuphyllophyta; Dermatophyta; Magnollophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Alzoaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-1998) to the EMBL; AB015183; BAA28779.1; SEQUENCE 790 AA; 86467 M
                                                                                                                                                      T2N18.14 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        germination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Expression
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                                                                                                                                                                                                                                                                             637
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                                                                                                                                                                                                                                                                                                                                         AGIWSEWSHPTAASTPRSERP--GPGGGVCEPRGGE---PSSGPVRR----ELKQFLGWL 71
                                                                                                                                                                                                                                                                                                 KKHAYCSNLSFRLYDOWRAWMOKSHKTRNOVGKLGEACVGGKGAE-----EERD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLAVEFRHPGWWEP--ERAEATRASLSALGASAVGTDMA--QRLPGSLPP
                                                                                                                                                                                                                                                                          SE----KNLRFLL-----QKVLK-QSDVGNLGRIVLPKKEAETHLPELEARD
                                                                                                                                                                                                                                                                                                                          AGNWYYWSHPPPL-PPQVSHPVGGPPPMVGQMQGLERAAPSGNGFQRQGGVEKKQ--GWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM
                                                                                                                                                                 9 (TrEMBLrel.
9 (TrEMBLrel.
9 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Vpl and 1. ";
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                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                    86467 MW;
                                                                                                                                                                                                                                                                                                                                                                                     33.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .J.;
water
                                                                                                                                                                  10,00
             BUELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                Created)
Last sequence
Last annument
            FUJII C.Y., SHEN M.,
BOWMAN C.L., RONNING
BUELL C.R., TOWN C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  channel
                                                                                                                                                                                                                                                                                                                                                                                      Score 76.5;
Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                    6FFE0075
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---WSHPT-AASTP---RSERPGP--
                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC32;
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                                                                                                                                                                              update)
                                                                                                                                                                  update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            databases
           , VANAKEN S.E.,
G C.M., BENITO M.
, NIERMAN W.C.,
                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
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                                                                                                                                                                                                                                                                           678
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                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                          636
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SOREA
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
AE2-2 ANION EXCHANGER (FRAGMENT).
                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                       179
                                                                                                                                                                                                                                                                                                                                                          120 GSGSASTWTSGSYGPGSASTWNPGSSQPGSSGPWTSGSSGLGSASTWNPGSSEPGSDGP- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3quus caballus (Horse)
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Arabidopsis thaliana chromosome II BAC T2N18 Submitted (MAR-1999) to the EMBL/GenBank/DDBJ EMBL; AC006260; AAD18149.1; ... SEQUENCE 297 AA; 33756 MW; 0921E56E CRC32;
                                                                                                                                                                                                                                                                 121 PGEQPP-QHRTLLSKHRTRGSC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. MAY-1999 (TIEMBLIE). 10, Last sequence update)
1. MAY-1999 (TIEMBLIE). 10, Last annotation update)
TBRINGGEN A-ALPHA CHAIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 25.6
mes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 itheria; Perissodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 KKAGIWSEWSHPTAASTP-----RSERPGP-----GGGVCEPRGGEPSSGPVRRELK 65
                                                                                                                                                                                                                             DGPQKPGSSGTLSTSIWTSGSSGPGSASTRHPGSSEPGSDGPRK 258
                                                                                                                                                                                                                                                                                                                          RRELKOFLGWLKKHAYCSNLSFRLYDQWRAWMOKSHKTRNOVGKLGEACVGGKGAEEERD 120
                                                                                                                                                                                                                                                                                                                                                                                          GSKKAGIWSEWSH-PTAAST--PRSERPGPGG--------GVCEPRGGEP-SSGPV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEPEEPEETRKEENQEEEASSCKSFTATPPRNAFLLTRCRS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QFLGWLKK----HAYCSNLSFRLYDQ-WRAWMQKSH-----KTRNQVGKLGEACVGGKGA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRCGWVKNAFPCHSFTGIIKPTCFSPVWRKWKSFSHASFSKKSEKRSSSSRSEPIFGRST 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tted (SEP-1998) to the AF095462; AAC67561.1; ER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KNASAAAETQEPTSPKVTCMGQVRINRSKKPKPETARVSGGATE-
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33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481
481 AA;
                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 76;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                    Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 76.5; D
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5B5EFF36 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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ı; Vertebrata; Archosauria;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                 --PRADGVRR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata; Mammalia;
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Best Local S
Matches 45
                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996
                                                                                                                                                                                                                                                                                                "Nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                          Acetobacter pasteurianus.
Plasmid pAP12875.
                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q44128
                                                   152 KHAARGARHIQRSSHCLPSGWQGQTGRMWDKSGVWPVAEALKFEFGNMAAYAAFRRL-MR
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. SEDLINE; 95309714.
                                                                                                                                                                                                                                                                                                                                                                     Acetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 561 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Variant AE2 anion exchanger transcripts types in the chicken gastric epithelium."
J. Biol. Chem. 271:8895-8902(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                       84 LYDQWRAWMQKSHKTRNQVGKLGEACVGGKGAEEERDPGEQP-PQHRTLLSKHRTR-GSC
                                                                          33 ASTPRSERPGPGGGVCEPRGGEPSSG------PVRRELKQFLGWLKKHAYCSNLSFR 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 96224107.
COX K.H., ADAIR-KIRK T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 GVQVGEARGAG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 GVR-REVRGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 RKKGVPKKGRKKRGRAAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FISSUE-PROVENTRICULUS (FORESTOMACH)
                                                                                                                                                                           Local Similarity
                                                                                                                                   1 GTVYFVQVRCNPFG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 EKDLNKALGVERFEEILSDAHPRSVEEPGRIYGEEDFEYHRQSSLHIHHPLSAHLPPDAR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 TRNOVGKLGEACVGGKGAEEERDPGEQPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RRELKQFLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
SYSKAQARVEMNAARSALVQAQGQA-GGGTARPTHSLPLSSPNPARKTMPVRERAQSGSA
                                                                                                      GAVYFAQEAVEAAGGPSAMEHRLVAVWTHLAASYGSQK---WSQTVKHIYDALGWSQYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVVPQGSGGVRTA--WIRGAHPARPSPAPSRPQPEPPAPG-----PASPPLAEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RCNPFGIYGSKKAGIWSEWSHPT----AASTPRSERPGPGGGVCEPRGGEPSSGPV----
                                                                                                                                                                                                                                                         U20550; AAA86883.1;
                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D48890; AAC59882.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity 23.6
45; Conservative
                                                                                                                                                                                                                                                                       :143-144(1995).
                                                                                                                                                                                                                                                                                                                                                                              Proteobacteria; alpha
                                                                                                                                                                                                                                 336 AA;
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155
                                                                                                                                                                                                                               36948 MW;
                                                                                                                                                                           8.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61186 MW; D1452E16 CRC32;
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                                                                                                                                                                                                                                                                                              a small plasmid isolated
                                                                                                                                                                                                                                                                                                            XU S.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    822
                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COX J.V.
                                                                                                                                                                          Score 75;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -PGENPPIEEGEEDEEEACDTETERSAEELRGG--PAE 182
                                                                                                                                                         Pred. No. 2.9;
7; Mismatches
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Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                               CF24DEA4 CRC32
                                                                                                                               -----IYGSKKAGIWSE------WSHPTA 32
                                                                                                                                                                                                                                                                                                                                                                            subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 AA
                                                                                                                                                                      DB 2;
2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                              82;
                                                                                                                                                                                                                                                                                                                                                                            Acetobacteraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -OHRTLLSKHRTRGSCPRAD 145
                                                                                                                                                                                     Length 336
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                                                                                                                                                                                                                                                                                              Acetobacter
                                                                                                                                                           48;
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                                                                                                       151
                                                   210
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                                                                                                                                                           10;
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142 --- PRA-DGVRREVRG 153 |:| || || 270 VGQPKAVSRVRSAARG 285

Search completed: September 16, 1999, 20:40:08 Job time: 5559 sec

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14.8 14.8

801 836

R11742 R14255

Clone Human

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ALIGNMENTS

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

protein search, using sw model

Run 92: September 17, 1999, 03:08:14; Search time 64.1 (without alignments) 102.726 Million cell updates/sec Seconds

Title: Perfect score: US-09-037-657-19 1505

PTLLIGSSLQATCSIHGDTP.......VYFVQVRCNPFGIYGSKKAG

278

Scoring table: 23686106 residues

BLOSUM62

Searched: 188963 seqs,

A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being print and is derived by analysis of the total score distribution. being printed

SUMMARIES

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Query Match Best Local

Length 413;

and survival. The perfer for cancers or The haemopoietin receptor (HR) NR6.1 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation differentiation and survival of a wide variety of cells. The HR and it derivatives can be used for modulating the activity of the receptors eto regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present N-PSDB; V27140:
New isolated haemopoletin receptor for modulating proliferation, diffe e.g. neuronal cells Novel haemopoietin receptor NR6.1 protein. Haemopoietin receptor; cell proliferation; cell differentiation; call survival; therapeutic; neuronal proliferation; drug screening; W55011 standard; Protein; 413 AA. W55011; herapeutics used for modulating (AMRA-) AMRAD OPERATIO (DZIE/) DZIEGLEWSKA H llexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y, Ojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson 1-SEP-1997; G02479. 29-SEP-1998 he haemopoietin receptor .aim 14; Page 77-81; 182pp; English -SEP-1996; AU-002246 98-260970/23. (first entry) velopment, maintenance or regeneration in an array of s and tissues in vitro and in vivo. They can be present in sed for modulating neuronal proliferation, differentiation The products can also be used for detection and diagnosis, as or predisposition to cancers, or for drug screening. ONS PTY LTD. aptor - used for developing products
differentiation and survival of cells, cell differentiation; cancer; feration,

밁 밁 밁 S . Q 밁 S Matches 278; Conservative 291 241 DDVSNQTSCRLAGIKPGTVYFVQVRCNPFGIYGSKKAG 278 231 DVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVV 181 171 111 121 61 ដ Local Similarity NYSLKYKLRWYGODNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTL PTILIGSSIQATCSIHGDTPGATAEGLYWTLNGBRLPSELSRLLNTSTLALALANUNGSR 60 DVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVV 240 NYSLKIKLRWYGQDNTČEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDYLTL QQSGDNLYCHARDGSILAGSCLYYGLPPEKPFNISCWSRNMKDLICRWTPGAHGETFLHT 120 DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAG QQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHT PTILIGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSR 100.0%; 0 Score 1505; DB 1; Pred. No. 8.8e-139; Mismatches Indels 0 Gaps 290 230 180 170 110 0,

W55012 standard; Protein; 425 W55012;

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PR New isolated haemopoietin receptor - used for developing products PT New isolated haemopoietin, differentiation and survival of cells, PT e.g. neuronal cells
PT e.g. neuronal cells
PT e.g. neuronal cells
PS Claim 15; Page 84-87; 182pp; English.

CC Interaction between the novel HR and a ligand facilitates proliferation, CC differentiation and survival of a wide variety of cells. The HR and it's CC derivatives can be used for modulating the activity of the receptors e.g.
CC to regulate development, maintenance or regeneration in an array of CC different cells and tissues in vitro and in vivo. They can be present in CC different cells used for modulating neuronal proliferation; differentiation come conserved in the products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
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Matches 278
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11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS P
(DZIE/) DZIEGLEWSKA H E.
            19-MAR-1998.
11-SEP-1997;
11-SEP-1996;
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Protein sequence of
Haemopoletin recepto
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opoietin receptor; cell
survival; therapeutic;
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1996; AU-002246.
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Conservative
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  receptor; cell proliferation;
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Pred. No. 9.2e-139;
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and survival.
e.g. for cance
Sequence 278
                       claim 17; Page 93-95; 182pp; English.

The protein sequence was generated by a 5N RACE of brain cDNA using NR6 specific primers. NR6 is a novel Haemopoietin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis,
                                                                                                                                                             for modulating proliferation, e.g. neuronal cells claim 17; Page 93-95; 182pp;
                                                                                                                                                                                                                               Zhang J;
WPI; 98-260970/23.
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           drug screening
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               DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAG
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hilarity 100.
Conservative
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Pred. No. 5e-139;
Mismatches 0
278
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23-JUL-1998.
15-JAN-1998; U00334.
16-JAN-1997; US-784863.
(GEMY) GENETICS INST IN
COllins M. Donaldson DD,
WPI; 98-414109/35.
                         N-PSDB; V41688.

New nucleic acid encoding U4 haematopoletin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease claim 9; Pages 26-27; 38pp; English.

This is the amino acid sequence of the murine U4 protein from the
                                                                                                                                                                                                                        26-OCT-1998 (first entry)
Nuclectide sequence of the murine
Nuclectine; depotein; haematopoietin
cell proliferation; immune respons
                                                                                                                                                                                                              autoimmune
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receptor superfamily, used in the methe modulation of cell proliferation,
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01-MAY-1998; U08865.

13-FEB-1998; US-074721.

01-MAY-1997; US-045287.

01-MAY-1997; US-850030.

13-FEB-1998; US-023890.
  The present sequence represents a Zcytor5 variant protein. Zcytor5 is a Cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
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                                                                                                                                                                                                                          (2YMO) ZYMOGENETICS INC.
Adams RL, FOSTET DC, Gilbert T,
Lok S, Presnell SR, Whitmore TE;
WPI; 99-034662/03.
                                                                                                                                                                  Claim 1; Page 83-84; 55pp;
                                                                                                                                                                                                                                                                                                                                                                     WO9849307-A1.
                                                                                                                                                                                                                                                                                                                                                                                               cardiac pathology; heart
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maintenance factor; thyroid; heart;
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                                                                                                                                                                                            New mammalian cytokinin-like receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sponse. Transformed mammalian cells are used to produce recombinant protein. The U4 protein is used to screen for specific binding yents, raise antibodies. It is also used as reagents for assays and stissue markers for isolation of cognate ligands and receptors, and pharmaceutical compositions which may modulate cell proliferation, all differentiation, and the immune system (e.g. for treating immune ificiency, inherited or the result of infection, autoimmune diseases,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 385
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Pred. No. 2.3e-138;
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Claim 1; Page 75-76; 55pp; English.

Claim 1; Page 75-76; 55pp; English.

Chief present sequence represents a protein designated Zcytor5; which a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or KNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.

Sequence 425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches 277
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Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
                                                                                                                                                                                       New mammalian cytokinin-like down-regulating Zcytor5 natur
                                                                                                                                                                                                                 N-PSDB; V70896.
                                                                                                                                                                                                                                                                                                 01-MAY-1997
                                                                                                                                                                                                                                                                                                               01-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                               Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                           cardiac pathology;
                                                                                                                                                                                                                                                                                                                                                                                                     Zcytor5; cytokinin-like receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat Zcytor5 protein
                                                                                                                                                                            in blood
                                                                                                                                                                                                                                                                                    13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                         01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W70862 standard;
                                                                                                                                                                                                                                                                                                                             3-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251
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                                                                                                                                                                                                                              99-034662/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVLDVVTTDPPPDVHVSRYGGLEDQLSVRWYSPPALKDFLFQAKYQIRYRVEDSVDWKVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTILIGSSLHATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSR
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                                                                                                                                                                                                                                                                                    US-850030
                                                                                                                                                                                                                                                                                                              US-074721.
US-045287.
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                                                                                                                                                                                                                                                                                                                                                                                        ; thyroid; heart; si
heart enlargement;
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                                                                                                                                                                                       natural
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Pred. No. 2
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                                                                                                                                                                                                                                                       Jelmberg
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                                                                                                                                                                                                                                                                                                                                                                                       down-regulation; gr
t; skeletal muscle;
ent; Zcytor5 ligand.
                                                                                                                                                                                                  Zcytor5
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                                                                                                                                                                                    detecting
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                                                                                                                                                                                                                                                       Lehner
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                                                                                                                                                                                useful for, e.g.
ting cardiotrophin-l
                                                                                                                                                                                                                                                                                                                                                                                                     growth factor;
e; cardiotrophin-1;
                                                                                                        the effect
                                        dies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                              in the
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Query Match Best Local Sim Matches 277;

Similarity

99.78;

Score 1500; I Pred. No. 2.86 0; Mismatches

DB 1; 2.8e-138; nes 1;

ç,

Gaps

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Length Indels

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PTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSR

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                                                                                                                                                                                                                                                                                                 Query Match
Best Local s
Matches 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1998; U08865.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a Zcytor5 variant protein. Zcytor5 is a cytokinin like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.

Sequence 389 AA;
            -131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ZYMO ) Z)
Adams RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in blood
Claim 1; Page 95-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mammalian cytokinin-like receptor Zcytor5 - down-regulating Zcytor5 natural ligands or detec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        maintenance factor; cardiac pathology; ]
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                                                         121
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       NYSLKYKLRWY
                                                                                     PTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSR 60
                                                                                                                                                                                DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3, Presnell SR, Whitmore 99-034662/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZYMOGENETICS INC.
L, Foster DC, Gilbert T,
L, Foster DC, Whitmore TE;
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytokinin-like receptor; down-regulation; nce factor; thyroid; heart; skeletal muscle
                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                  97.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                       Score 1464; DB 1;
Pred. No. 8.1e-135;
4; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or5 - useful for, e.g.
detecting cardiotrophin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lehner
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                                                                                                                                                                                                                                                                                                                                       Length 389;
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190
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or immune response, for treating trunce.

PS Claim 9; Pagees 29-30; 38pp; English.

CC This is the amino acid sequence of the human U4 protein from the CC haematopoletin receptor superfamily, used in the method of the CC invention for the modulation of cell proliferation, or the immune CC response. Transformed mammalian cells are used to produce recombinant CC U4 protein. The U4 protein is used to screen for specific binding CC agents, raise antibodies. It is also used as reagents for assays and CC as tissue markers for isolation of cognate ligands and receptors, and CC cell differentiation, and the immune system (e.g. for treating immune antipolic compositions which may modulate cell proliferation, in the immune system (e.g. for treating immune antipolic contributions of infection, autoimmune diseases,
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                                                                                                                                                                                                                                                                                                                                                                                                              or immune response, for treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collins M, Donaldson WPI; 98-414109/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; V41689
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16-JAN-1997; US-784863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune
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of the human U4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune response; antibody;
cancer; allergy.
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חס, Neben
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ody; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                              receptor superfamily ting cell proliferation auto:immune disease
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                                                                                                                            DVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVV
                                                             NYSLKYKLRWYGODNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTL
                                                                                            QQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWIDGAHGETFLHT
                                                                      NYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTL
                                                                                                                                                                       Similarity
                                                                                                                                                               Conservative
                                                                                                                                                                     97.2%;
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                                                                                                                                                             Score 1463; DB Pred. No. 1.1e-15; Mismatches
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.1e-134;
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Length 408;

RESULT W70840

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E Human Zcytor5 variant.

2 Cytor5; cytokinin-like receptor; dow maintenance factor; thyroid; heart; s) cardiac pathology; heart enlargement; Homo sapiens.

W09849307-A1.
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Best Local Similarity
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13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a Zcytor5 variant protein. Zcytor5 is a Cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
                                                                         W70844 standard; Protein; W70844; 17-MAR-1999 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l;
cardiac pathology; heart enlargement; Zcytor5 ligand; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 81-82; 55pp;
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                                                                                                                                                          Homo sapiens
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                             -like receptor; down-regulation; gro;
; thyroid; heart; skeletal muscle; o
heart enlargement; Zcytor5 ligand;
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ed. No. 1e-134;
Mismatches 5;
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Best Local s
Matches 268
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                                   01-MAY-1998; U08865.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
                                                                                                                                                          17-MAR-1999 (first entry)
Human Zcytor5 variant.
Zcytor5; cytokinin-like re-
(ZYMO
Adams
Lok S,
                                                                                                                              Zeytox5; cytokinin-like receptor; d.
maintenance factor; thyroid; heart;
cardiac pathology; heart enlargemen
Homo sapiens.
                                                                                                  05-NOV-1998
                                                                                                                                                                                                            W70845 standard;
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down regulating Zcytor5 natural ligands or det
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ZYMOGENETICS INC.

L, Foster DC, Gilbert
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Similarity 96.4%;
68; Conservative
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                                                                                                                                    receptor; down-regulation; growth old; heart; skeletal muscle; cardi enlargement; 2cytor5 ligand; vari
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Best Loc
Matches
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01-MAY-1998; U08865.

13-FEB-1998; US-074721.

01-MAY-1997; US-045287.

01-MAY-1997; US-850030.

13-FEB-1998; US-022890.

(ZYMO) ZYMOGENETICS INC.

Adams RL, FOSTET DC, G111

LOK S, Presnell SR, Whitm
                                     in blood
Claim 1;
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The present sequence represents an allelic varaint of Zcytor5, which is a cytokinin-like receptor. Soluble administered to down-regulate the effects of a growth
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                                                   New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
                                                                                                                                                                                                    Homo sapiens.
WO9849307-A1.
                                                                                N-PSDB; V70895
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;, Gilbert
Whitmore
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Pred. No. 7e-135;
5; Mismatches
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                                                                                                             Jelmberg
                                                                                                                                                                                                                                              down-regulation;
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aint of protein designated 
pluble Zcytor5 may be 
growth and/or maintenance
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be administered
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Best Loc
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05-NOV-1998.
01-MAY-1998; (
13-FEB-1998; (
01-MAY-1997; (
      The present sequence represents a Zcytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNN or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
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                                                                                                                                                                                                                                                                                                                                                    (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
                                                                                                                                                                                                                                                                                                                                     Lok S, Presnell SI WPI; 99-034662/03
                                                                                                                                                                                                                                                    Claim 1; Page
                                                                                                                                                                                                                                                                          down-regulating in blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiac pathology;
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+ skeletal muscl
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e; cardiotrophin-1;
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cardiotrophin-l
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Matches 267; Conser
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01-MAY-1998; U08865.

13-FEB-1998; US-074721.

01-MAY-1997; US-045287.

01-MAY-1997; US-850030.

13-FEB-1998; US-023890.
                                                                                                       The present sequence represents a Zcytor5 variant protein. Zcytor5 is a Cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome ly. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Zcytor5 variant.

Human Zcytor5 variant.

Zcytor5; cytokinin-like receptor; down-regulation;
maintenance factor; thyroid; heart; skeletal muscle

cardiac mathology; heart enlargement; Zcytor5 ligar
                                                                                                                                                                                                                                                                                     Claim 1; Page 98-99;
                                                                                                                                                                                                                                                                                                        New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
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PTLLIGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSR 60
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                                                                                                                                                                                                                                                                                                                                               ) ZYMOGENETICS INC.
RL, Foster DC, Gilbert T, Jelmberg AC,
Presnell SR, Whitmore TE;
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267; Conserv
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96.0%;
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                                                     Score 1461;
Pred. No. 1
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Pred. No. 1
                                          Mismatches
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..6e-134;
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                                                                                                                                                                                      PS Claim 1; Page 89-90; 55pp; English.

CC The present sequence represents a Zcytor5 variant protein. Zcytor5

CC is a cytokinin-like receptor. Soluble Zcytor5 may be administered to

CC down-regulate the effects of a growth and/or maintenance factor in

CC thyroid, heart, and skeletal muscle for example to lessen the effect

CC of cardiotrophin-l on cardiac pathologies, so preventing heart

CC enlargement. Zcytor5 could be used to detect cardiotrophin-l in the

CC blood, and to discover other possible Zcytor5 ligands. A probe

CC comprising Zcytor5 DNA or RNA can be used to determine the presence

and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the

CC anti-lidotypic antibody could be used to purify Zcytor5 and

CC therapeutically to modify Zcytor5 ligand effects.
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Best Local Similarity 96.0%;
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13-FEB-1998; US-074721.

01-MAY-1997; US-045287.

01-MAY-1997; US-850030.

13-FEB-1998; US-023890.

(ZYMO ) ZYMOGENETICS INC.

Adams RL, FOSTET DC, Gilbert T, Je

Lok S, Presnell SR, Whitmore TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Zcytor5 variant
Zcytor5; cvtov'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiac pathology; heart enlargement;
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QRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGSHGETFLHT
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                                                                                                                   Conservative
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Pred. No. 2e-134;
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cardiotrophin-l
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Copyright (c) 1993 - 1998. Compugen
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US-07-676-647-2
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FIG RYY	178 LILDVLDVYTTDPPPDVHYSRVGGLEDQLSVRWYSP : : : : : : : : : :	118 LHTNYSLKYKLKWYGQDNTCEEYHTV :: : : 154 LETNETLKSEWATHKFADCKAKRDT-	9 9	1 PTILIGSSIQATCSIHG	Query Match Best Local Similarity 28. Matches 77; Conservative	TOPOLOGY: linear MOLECULE TYPE: protein 07-797-556-2	SEQUENCE CHARACTERISTICS: LENGTH: 708 amino acids TYPE: AMINO ACID	TELEFA:	ISTRATION NUM ERENCE/DOCKET OMMUNICATION	ON: 435 INFORMATI , Kathryn	RENT APPLI PPLICATION ILING DATE	COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patenti	WA RY: USA 98101 READABLE FORM	Immunex 1 Universi	TION: TION: ENCES:	07-797-556-2 07-797-556-2 equence 2, Application atent No. 5262522 GENERAL INFORMATION:		40 135.5 9.0 888 41 134 8.9 229 42 133.5 8.9 719 43 133.5 8.9 719 44 133.5 8.9 1452 45 132 8.8 230
HVERIAITARARA TOO	DYHYSRYGGLEDQLSYRWYSPPALKDFLFQAKYQIRYRYEDSYDW 	LHTNYSLKYKLRWYGODNTCEEYHTVGDHSCHIPKDLALFTPYEIWVEATNRLGSARSDV 	GSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNNKDLTCRWTPGAHGETF	PTLLIGSSLOATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLN : : : : : : : : : : : : : : : :	3%; Score 290; DB 1; Length 3%; Pred. No. 1.2e-21; 47; Mismatches 136; Indel		Ω.	2:	BER: 32,172 NUMBER: 2607 INFORMATION:	••	797,556	py d.sk compatible PC-DOS/MS-DOS n Release #1.0, Version #1.25		: Corporation ty Street	David P. Receptor for Oncostatin M and Leu Inhibitory Factor 17	US/07797556	ALIGNMENTS	1 US-08-445-640-35 2 US-08-684-687-2 1 US-07-943-843-4 2 US-08-347-003-4 2 US-08-52-971-4 3 PCT-US93-09636-6
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270 SQIPPEDTASTRSSFTVQDLKPFTEYVFRIRC 301
                                 238 KVV---DDVSNQTSCRLAGLKPGTVYFVQVRC 266
                                                                 212 INFOPVYKVKPNPPHNLSVINSEELSSILKLTWTN-PSIKSVII-LKYNIQYRTKDASTW 269
                                                                                                  178 LTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDW 237
                                                                                                                                      154 LETNFTLKSEWATHKFADCKAKRDT--PTSCTVDYSTVYFVNIEVWVZAENALGKVTSDH 211
                                                                                                                                                                       118 LHTNYSLKYKLRWYGODNTCEEYHTVGPHSCHIPKDLALETPYEIWVEATNRLGSARSDV 177
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                                                                                                                                                                                                           96 SLNIQLTCNILTEGQLEQNYYGITIISGLPPEKPKNLSCIVNEGKKMRCEWDGGR--ETH 153
                                                                                                                                                                                                                                              58 GSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETF 117
                                                                                                                                                                                                                                                                                36 PVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVTFTDIA 95
                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                   1 PTLLIGSSLOATCSIHG---DTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLN 57
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270 SQIPPEDTASTRSSFTVQDLKPFTEYVFRIRC 301
                                      238 KVV---DDVSNQTSCRLAGLKPGTVYFVQVRC 266
                                                                                                                178 LTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDW 237
                                                                                                                                                         154 LETNFTLKSEWATHKFADCKAKRDT--PTSCTVDYSTVYFVNIEVWVEAENALGKVTSDH
                                                                                                                                                                                            118 LHTNYSLKYKLRWYGODNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                                                                 96 SLNIQLICNILTFGQLEQNYYGITIISGLPPEKPKNLSCIVNEGKKMRCEWDGGR--ETH 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                        58 GSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETF 117
                                                                                                                                                                                                                                                                                                               36 PVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVTFTDIA 95
                                                                                                                                                                                                                                                                                                                                                        1 PTLLIGSSLQATCSIHG---DTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLN 57
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                                                                           INFOPVYKVKPNPPHNLSVINSEELSSILKLTWTN-PSIKSVII-LKYNIQYRTKDASTW
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MEDIUM TYPE: Floppy disk
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                                                                                                    169 RLGSARSDVLTLDVLDVV----
                                                                                                                                                               114 GETFLHTNYSLK-YKLRWYGQ---DNTCEEYHTVGPHSCHIP-KDLALFTPYEIWVEAIN 168
                               221 FQAKYQIRYRVE-DSVDWKVVDDVSNQT-SCRLAGLKPGTVYFVQVRC 266
                                                                                                                                                                                                 94 HTQA----FLSCCLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLICQWEPGP- 149
                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                   1 PTLLIGSSLOATCSIHGDTPGATAE-GLYWTLNGRRLPSELSRLLN--TSTLALALANLN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OR APPLICATION DATA:
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                                                                                                                                                                                                                                  GSRQQSGDNLVCHARDGS---ILAGSCLYVGLPPEKPFNISC-WSRNMKDLTCRWTPGAH 113
INOKCELRHKPORGEASWALVGPLPLEALQYELCGLLPATAYTLQIRC 309
                                                               ALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEAAPPQAGCLQ----LCW--EPWQPGLH 261
                                                                                                                                  -ETHLPTSFTLKSFKSRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLYQNMGIWVQAEN
                                                                                                                                                                                                                                                                     PIVHLGDPITASCIIKQNCSHLDPEPQILWRLGAELQPGGRQQRLSDGTQESIITLPHLN 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hellwege, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/07923976
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22-MAR-1991
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in Release #1.0, Version #1.25
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Pred. No.
                                                                                                -TTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFL
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Best Local
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221 FQAKYQIRTRYE-DSYDWKYYDDVSNQT-SCRLAGLKPGTVYFVQVRC
                                                                                         169 RIGSARSDVLTIDVLDVV-----TTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFL 220
                                                                                                                                                            114 GETFLHTNYSLK-YKLRWYGQ---DNTCEEYHTVGPHSCHIP-KDLALFTPYEIWVEATN 168
                                                                                                                            149 -ETHLPTSFTLKSFKSRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLYQNMGIWVQAEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
RIOR APPLICATION DATA:
                                                                                                                                                                                                                                       58 GSRQQSGDNLVCHARDGS---ILAGSCLYVGLPPEKPFNISC-WSRNMKDLTCRWTPGAH 113
                                                                                                                                                                                                                                                                           34 PIVHLGDPITASCIIKQNCSHLDPEPQILWRLGAELQPGGRQQRLSDGTQESIITLPHLN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIOR APPLICATION DATA:
                                                                                                                                                                                                   94 HTQA----FLSCCLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLICQWEPGP- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 74
FILING DATE: 23-MAR-1990
                                                                                                                                                                                                                                                                                                              1 PTILIGSSIQATCSIHGDTPGATAE-GLYWTLNGRRLPSELSRLLN--TSTLALALANIN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR APPLICATION DATA:
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                                                     ALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEAAPPQAGCLQ----LCW--EPWQPGLH
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Fukunaga, Rikiro
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Colony-Stimulating Factor Receptor
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262 INQKCELRHKPQRGEASWALVGPLPLEALQYELCGLLPATAYTLQIRC 309

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                                                                         149
                                                                                                         114 GETFLHTNYSLK-YKLRWYGO---DNTCEEYHTVGPHSCHIP-KDLALETPYEIWVEATN 168
                                  169 RLGSARSDVLTLDVLDVV------TTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFL
208 ALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEAAPPQAGCLQ----LCW--EPWQPGLH 261
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                                                                                                                                              94 HTQA----FLSCCLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLICQWEPGP- 149
                                                                                                                                                                                    58
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                                                                                                                                                                                                                       34 PIVHLGDPITASCIIKQNCSHLDPEPQILWRLGAELQPGGRQQRLSDGTQESIITLPHLN 93
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                                                                                                                                                                                                                                                        1 PTILIGSSIQATCSIHGDTPGATAE-GLYWTLNGRRLPSELSRLLN--TSTLALALANLN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELEPHONE:
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                                                                       -ETHLPTSFTLKSFKSRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLYQNMGIWVQAEN 207
                                                                                                                                                                                 GSRQQSGDNLVCHARDGS---ILAGSCLYVGLPPEKPFNISC-WSRNMKDLTCRWTPGAH 113
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Artington
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                                                                                                                                                                                                                                                                                                                Score 222; DB 1;
Pred. No. 1.6e-14;
                                                                                                                                                                                                                                                                                              Mismatches
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116 TFLHTNYSLK-YKLR----WYGQDNTCEEYHTVGPHSCHIP-KDLALFTPYEIWVEATNRL 170

THLPTSFILKSFRSRADCQYQGDTIPDCVAKKRQNNCSIPRKNLLLYQYMAIWVQAENML

210

----PDVHVSRVGGLEDQLSVRWVS-PPALKDFLF 221

34 PVVRLGDPVLASCTISPNCSKLDQQAKILWRLQDEPIQPGDRQHHLPDGTQESLITLPHL

NGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSR-NMKDLTCRWTPGAHGE 115

NYT-QAFLFCLVPWEDSVQLLDQAELHAGYPPASPSNLSCLMHLTTNSLVCQWEPGP--E

150

93

PTILIGSSIQATCSIHGDTPGATAEG-LYWTLNGRRL-PSELSRLL--NTSTLALALANL 56

171 GSARSDVLTLDVLDVVTTDPP----

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Matches

83;

Conservative

28.9%;

Score 221.5; DB Pred. No. 1.7e-14 5; Mismatches 12

Indels Length

31;

Gaps

14;

DB 1;

Query Match Best Local Similarity

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; MOLECULE TYPE: US-07-923-976-2
                                                                                                   NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                SEQUENCE CHARACTERISTICS
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                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                 ECOMMUNICATION INFORMATION: 703-415-1500
                                                                                                                                                                   EFERENCE/DOCKET NUMBER:
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                                                  AMINO ACID
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P.O. Box 2266 Eads Station
                                                                                                                    703-415-1508
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn
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                                                                amino acids
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                protein
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                                                                                                                                                                                                                                 2-MAR-199
                                                                                                                                                                                                James
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version
                                                                                                                                                                                                                                                 PCT/JP91/00375
                                                                                                                                                                                                                                                                                                JP 176629/1990
                                                                                                                                                                                                                                                                                                                                            JP 74539/1990
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193 DVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVE-DSVDWKVVDDVSNQT-SCR 250
                                                                         142 TVGPHSCHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVV------TTDPPP 192
                                      61 KDGQSHCCIPRKHLLLYQNMGIWVQAENALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSP 120
                                                                                                                                                     87 PPEKPFNISC-WSRNMKDLTCRWTPGAHGETFLHTNYSLK-YKLRWYGQ---DNTCEEYH 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 EQECELRYQPQLKGANWTLVFHLPSSKDQFELCGLHQAPVYTLQMRC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 QAKYQIRYRVE-DSVDWKVVDDV-SNQTSCRLAGLKPGTVYFVQVRC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 GSSESPKLCLDPMDVVKLEPPMLQALDIGPDVVSHQPGCL-
                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32142
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ECULE TYPE: protein
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                                                                                                                    PPAIPHNLSCLMNLTTSSLICQWEPGP--ETHLPTSFTLKSFKSRGNCQTQGDSILDCVP 60
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07110-1199
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32.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                 /note= "Represents residues 98 to
731 of human granulocyte colony-stimulating
factor-receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 08/094,713
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                                                                                                                                                                                                                   Score 199; DB 2;
Pred. No. 2.2e-12;
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Best Local S
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                                                                                                                                                                                       146 HSCHIPKDLALFTPYEIWVEATNRLGSARSDYLTLDVLDVVTTDPPPDVHVSRVGGLEDQ 205
206 LSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 LCGLLPATAYTLQIRC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 LAGLKPGTVYFVQVRC 266
                                                                                                           57
                                                                                                                                                                                                                                                                                             1 LPPEKPKNLSCIVNEGKKMRCEWDGGR--ETHLETNFTLKSEWATHKFADCKAKRDT--P 56
                                                                                                                                                                                                                                                                                                                                                                                         86 LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 EAAPPQAGCLQ----LCW--EPWQPGLHINQKCELRHKPQRGEASWALVGPLPLEALQYE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                     TSCTVDYSTVYFVNIEVWVEAENALGKVTSD----
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1..572
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   742 of human gp130."
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Pred. No. 7
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Best Local (
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                                                                                                                                             141 VACTWERGR--DTHLYTEYTLQLSGPKNLTWQKQCKDIYC-DYLDFGINLTPESPESNFT 197
                                                                                                                                                                               104 LTCRWTPGAHGETFLHTNYSLKY----KLRWYGQ--DNTCEEYHTVG------PHSCHI 150
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                                   211 VSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQV 264
                                                                         198 AK---
                                                                                                                                                                                                                     95
                                                                                                                                                                                                                                                     45 NTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMK-D 103
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                                                                                                                                                                                                                                                                                                                             3 LLIGSSLQATCSIHGDTPGATAEGLYWTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECOMMUNICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECULE TYPE:
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                                                                                                         PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRW 210
                                                                                                                                                                                                                     GTTLFVCKLACINSDEIQ
                                                                                                                                                                                                                                                                                       ILLGSTVNITCSL-----KPRQGCFHYSRRNKLILYKFDRRINFHHGHSLNSQVTGLPL 94
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-RDEGLYLLNRLRYRPSNSRLWNMYNVTKAKGRHDLLDLKPFTEYEFQI 294
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Presky, David H
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                                                                       VTAVNSLGSSSSLPSTFTFLDIVRPLPPWDIRIKFQKASVSRCTLYW
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                                                                                                                                                                                                                                                                                                                                                                                    Score 178; 1
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                                                                                                  151 PKDLALFTPYEIWVEATNRLGSARSDYLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRW 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFORMATION FOR
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                                                                                                                                    141 VACTWERGR -- DTHLYTEYTLQLSGPKNLTWQKQCKDIYC - DYLDFGINLTPESPESNFT 197
                              211 VSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQV 264
                                                                   198 AK-----VTAVNSLGSSSSLPSTFTELDIVRPLPPWDIRIKFQKASVSRCTLYW
                                                                                                                                                                       104 LTCRWTPGAHGETFLHTNYSLKY----KLRWYGQ--DNTCEEYHTVG-----PHSCHI 150
                                                                                                                                                                                                                                          45 NTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMK-D 103
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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-----RDEGLYLLNRLRYRPSNSRLWNMVNVTKAKGRHDLLDLKPFTEYEFQI 294
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24.8%;
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RESULT 12 US-07-865-878A-4

Sequence 4, Application US/07865878A

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Sequence 2, App.
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                    174 RSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKD-FLFQAKYQIRYRVE 232
                                                                                                   250 ILDOWOHV-ELSDGTAHTITDAYAGKEYIIQV 280
                                                                                                                                    233 DSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQV 264
                                                                                                                                                                   190 NATAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTWQTPSTWPDPESFPLKFFLRYRPL 249
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                                                                                                                                                                                                                                                                                                                                   65 DNLYCHARDGSILAGS-CLYYGLPPEKPFNISCWSRNM-KDLTCRW-----TPGAHGE 115
                                                                                                                                                                                                                                                                                                     85 GLYACTHRDSWHLRHQVLLHVGLPPREPV-LSCRSNTYPKGFYCSWHLPTPTYIPNTFNV 143
                                                                                                                                                                                                                                                                                                                                                                     38 LGSDVTLPCGTANWDAAVT-----WRVNGTDLAPD---LLNGSQLV-----LHGLELGHS 84
                                                                                                                                                                                                                                                                                                                                                                                                   5 IGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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LEPHONE: 212 790-9090
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                                                                                                                                                                                                                                                                                                                                                                                                                                           73;
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10036-271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                         123;
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Application US/07676647

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Davis

Samuel

The Ciliary Neurotrophic Factor Receptor

Z, Application US/08449329 5648334

Davis, Samuel

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US-07-676-647-2
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Best Local S
Matches 73
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250 ILDQWQHV-ELSDGTAHTITDAYAGKEYIIQV 280
                                    233 DSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQV 264
                                                                          190 NATAITEDEETIVKPDPPENVVARPVPSNPRRLEVTWQTPSTWPDPESEPLKFELRYRPL
                                                                                                                                                         144 TVLHGSKIM--
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                                                                                                                                                                                                                                                                                                             38 LGSDVTLPCGTANWDAAVT-----WRVNGTDLAPD---LLNGSQLV-----LHGLELGHS
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                                                                                                                 RSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKD-FLFQAKYQIRYRVE 232
                                                                                                                                                                                          TFLHTNYSLKYKLRWYGODNTCEEYHTVGPHSCHIPKDLALFT--PYEIWVEATNRLGSA 173
                                                                                                                                                                                                                                                                                                                                                   IGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSG 64
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EPHONE: 212 790-9090
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity 26.8
73; Conservative
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                                                                                                                                                       --VCEKDPAL-KNRCHI-RYMHLFSTIKYKVSISVSNALGH- 190
                                                                                                                                                                                                                                                                                                                                                                                          Score 172.5;
Pred. No. 6e-1
35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            6e-10;
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NUMBER OF SEQUENCES:

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1155 Avenue of

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                                                                                                                                                     08-445-073-2
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                            174 RSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKD-FLFQAKYQIRYRVE 232
                                                                                                                                                                                                                                                                                                                                                                                                  116 TFLHTNYSLKYKLRWYGODNTCEEYHTVGPHSCHIPKDLALFT--PYEIWVEATNRLGSA 173
                                                                                                                                                                                                                      250 ILDQWQHV-ELSDGTAHTITDAYAGKEYIIQV 280
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                                                                                                                                                                                                                                                                                          190 NATAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTWQTPSTWPDPESFPLKFFLRYRPL 249
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APPLICATION NUMBER: US 0
FILING DATE: 15-MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 DNLVCHARDGSILAGS-CLYVGLPPEKPFNISCWSRNM-KDLTCRW-----TPGAHGE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 LGSDVTLPCGTANWDAAVT-----WRYNGTDLAPD---LLNGSQLV-----LHGLELGHS 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 IRRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                    rancopouros,
                                       Furth, Mark E
                                                                           Davis, Samuel
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los, George D.
The Ciliary Neurotrophic Factor Receptor
                                                          Stephen P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 172.5;
Pred. No. 6e-1
35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6526-065
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                174 RSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKD-FLFQAKYQIRYRVE 232
                                                                                                                                             144 TVLHGSKIM-
                                                                                                                                                                       116 TFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFT--PYEIWVEATNRLGSA 173
                                                                                                                                                                                                            85 GLYACFHRDSWHLRHQYLLHVGLPPREPV-LSCRSNTYPKGFYCSWHLPTPTYIPNTFNV 143
                                                                                                                                                                                                                                            65 DNLVCHARDGSILAGS-CLYVGLPPEKPFNISCWSRNM-KDLTCRW-----TPGAHGE 115
                                                                                                                                                                                                                                                                                   38 LGSDVTLPCGTANWDAAVT----WRVNGTDLAPD---LLNGSQLV-----LHGLELGHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US OF FILING DATE: 28-MAR-1991
                                                                                                                                                                                                                                                                                                                   5 IGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELEPHONE: 212 790-9090
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                               DSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQV 264
ILDQWQHV-ELSDGTAHTITDAYAGKEYIIQV 280
                                                                   NATAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTWQTPSTWPDPESFPLKFFLRYRPL
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: New York
:RY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                           11.5%; Score 172.5; DB 2; 26.8%; Pred. No. 6e-10;
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                                                                                                                                                                                                                                                                                                                                                                                           Length 372;
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Gaps

14;

84

completed: September 16, 1999, 20:41:09 me: 5438 sec

OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:09;)9 ; Search time 49.27 Seconds
(without alignments)
226.065 Million cell updates/sec

Title: Perfect score: US-09-037-657-19 1505

Sequence: 1 PTILIGSSLQATCSIHGDTP......VYFVQVRCNPFGIYGSKKAG 278

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database : PIR_60:* pir1: * pir2: *

and is No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, serived by analysis of the total score distribution.

SUMMARIES

Result No.

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147.5	151	154.5	154.5	156	158.5	
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 leukemia inhibitor	somatotropin recep	interleukin-6 rece	interleukin-6 rece	leptin receptor, i	interleukin-6 rece	

ALIGNMENTS

prolactin receptor long form precursor, hepatoma and breast cancer cells - human C;Species: Homo sapiens (man) C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998

dery, M.; Shirota, M.; Jolicoeur, C.; Lesueur, L.; Ali, S.; Gould, 3, 1455-1461, 1989

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R:Fuh, G.; Wells, J.A. J. Biol. Chem. 270, 13133-13137, 1995 A;Tille: Prolactin receptor antagonists that inhibit the growth of breast cancer cel. A;Reference number: A57018; MUID:95286597 A;Accession: A57018 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-206 <res> A;Cross-references: GB:S78505; NID:g999114; PID:g999115</res>	RESULT 2 A57018 prolactin receptor - human (fragment) C;Species: Homo sapiens (man) C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996 C;Accession: A57018	QY 249 CRLAGLKPGTVYFVQVRCNP 268 ::	QY 194 VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTS 248	OY 135 NTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPD 193	OY 76 ILAGSCLYVG-LPPEKPENISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 134 :	Query Match 20.5%; Score 308.5; DB 2; Length 622; Best Local Similarity 38.5%; Pred. No. 2.4e-20; Matches 77; Conservative 27; Mismatches 85; Indels 11; Gaps 7;	C:Keywords: 9lycoprotein; transmembrane protein F:1-24/Domain: signal sequence #status predicted <sig> F:25-622/Product: prolactin receptor, long form #status predicted <mat> F:59;104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted</mat></sig>	A; Genetics: A; Gene: GDB:PRLR A; Gross-references: GDB:120315; ONIM:176761	A;MOLECULE Type: mRNA A;Residues: 1-622 <bou> A;Cross-references: GB:M31661; NID:g190361; PID:g190362</bou>	A;Title: Identification of a cDNA encoding a long form of prolactin receptor in hum A;Reference number: A40144; MUID:90114212 A;Accession: A40144

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              A;Status: preliminary; translated
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C;Species: Columba livia (domestic pigeon)
C;Bate: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
C;Accession: IS0455
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                                                                                                                                                      Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:U07694; NID:g466381; PID:g466382
                                                                                                                                    Date: 02-Aug-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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Title: Cloning, expression, and mutational analysis of the
Reference number: I50455; MUID:94283267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: mRNA Residues: 1-830 <CHE>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                   EDQLSVRWVSPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                          HSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDV--HVSRVGGL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPEKPTIIKCRSPEKETFTCWWKPGSDGG---HPTNYTLLYSKEGEERVYECPDYKTAGP 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPEKPFNISCWSRNMKDLICRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP 145
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mRNA
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ilarity 39.2%;
Conservativė 2
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                from GB/EMBL/DDBJ
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Pred. No. 2.2e-20;
5; Mismatches 80
                                                                                                                                    02-Aug-1996
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                                                                                                                                  #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M22959; NID:g200481; PID:g200482
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-292 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (01. Endocrinol. 3, 674-680, 1989
(v71tle: Expression of multiple forms of
vReference number: 157699; MUID:89261824
v/Accession: 177525
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
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Best Local :
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                                272 YGSK 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 ALKDF---LFQAKYQIRYRYEDSVDWKVVDDYSNQTSCRLAGLKPGTVYFVQVRCNPFGI
                                                                                                                             91 WKIYIITVNATNEWGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP
                                                                                                                                                                                              35 DKETFTCWWNPGSDGG---LPTNYSLTYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI
                                                                                                                                                                                                                                                                                            40 LSRLLNTSTLALALANLNGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 LSRLLNTSTLALALANINGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSR 99
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                                                                                          ALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 271
                                                                                                                                                            FTPYEIWVEATURLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVS--PP
                                                                                                                                                                                                                          NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNT--CEEYHTVGPHSCHIPKD-LAL 156
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YWSR 212
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37; Mismatches
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Pred. No. 3.
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Pred. No. 3.7e-19;
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prolactin receptor,

long form

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R;Hlbi, M.; Murakami, M.; Saito, M.; Hirano, T.;
Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of an
A;Reference number: A36337; MUID:91084844
                                                                                                                                                               membrane glycoprotein gp130 precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998
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                                            A; Accession: A36337
                                                                                                                                                         Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: mRNA
Residues: 1-557, 'F', 559-608 <EDE>
Residues: 1-557, 'F', 559-608 <EDE>
Cross-references: EMBL:X73372; NID:g312696; PID:g312697
Comment: Prolactin receptor have long form and short form which are Comment: This long form receptor is capable of transducing a signal skeywords: receptor; transmembrane protein
;230-253/Domain: transmembrane #status predicted <TMM>
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Best Local
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Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
bmitted to the EMBL Data Library, June 1993
Description: Isolation and nucleotide sequence of a mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title: Changes in prolactin receptor expression Reference number: I53269; MUID:93307149 Accession: I53269
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Residues: 1-608 <MOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title: Cloning and sequencing of the cDNA encoding the Reference number: JT0671; MUID:94085788 Accession: JT0671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Mus musculus (house mouse)
Date: 02-Aug-1996 #sequence_revision
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Residues: 1-608 <RES>
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preliminary
e type: mRNA
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                                                                                                                                                                                                                                                                                                                               YWSR 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP
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    Conservative

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Pred. No. 9.3e-19;
37; Mismatches 85
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                                                                                                                              T.; Taga,
                                                                               IL-6 signal transducer, gp130
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C;Accession: A3431
R;Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.;
R;Zhang, R.; Buczko, E.; Tsai-Morris, C.H.; Hu, Z.Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: M34083; A; Note: the authors translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-610 <ZHA>
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A; Accession: A34631
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A;Map position: 5q11-5q11
C;Keywords: glycoprotein;
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C;Genetics:
A;Gene: GDB:IL6ST; GP130
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Best Local S
Matches 76
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Best Local Sim
Matches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Rattus norvegicus (Norway rat)
Date: 13-Jul-1990 #sequence_revision 09-Oct-1992 #text_change 10-Sep-1997
                                                                                                   192 PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWXVVDDVSNQ 246
                                                                                                                                                                                             135 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP 191
                                                                          126 RNLTL-EVKOLKOKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHO
184 TOFKVFDLYPGOKYLVQTRCKPDHGYWSR
                                        247 TSCRLAGLKPGTVYFVQVRCNPFGIYGSK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 KVV---DDVSNQTSCRLAGLKPGTVYFVQVRC 266
                                                                                                                                                         66 TTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP
                                                                                                                                                                                                                                       15 SILKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 SQIPPEDTASTRSSFTVQDLKPFTEYVFRIRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 INFDPVYKVKPNPPHNLSVINSEELSSILKLTWTN-PSIKSVII-LKYNIQYRTKDASTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 LTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 LHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDV 177
                                                                                                                                                                                                                                                                                        75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 SLNIQLTCNILTFGQLEQNVYGITIISGLPPEKPKNLSCIVNEGKKMRCEWDGGR--ETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 GSRQQSGDNLYCHARDGSILAGSCLYYGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 PVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVTFTDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 19.38;
Local Similarity 28.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PTILIGSSLOATCSIHG----DTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLN 57
                                                                                                                                                                                                                                                                             SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LETNFTLKSEWATHKFADCKAKRDT--PTSCTVDYSTVYFVNIEVWVEAENALGKVTSDH
                                                                                                                                                                                                                                                                                                                              Similarity
76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDB:126725; OMIM:600694
                                                                                                                                                                                                                                                                                                                                           19.2%; Score 288.5; DB 2 36.4%; Pred. No. 1.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                          NID:g205122; PID:g205123
the codon GAG for residue 533 as
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Pred. No. 2e-18;
7; Mismatches 13(
                                                                                                                                                                                                                                                                                                                          Mismatches
212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A36116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Expression of two forms of prolactin receptor in rat ovary and liver. A; Reference number: A36116; MUID:91155946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prolactin receptor 2 precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Rattus norvegicus (Norway rat)
Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 10-Sep-1997
Accession: A41070; I55417
Ali, S.; Pellegrini, I.; Kelly, P.A.
                                                                                              Query Match
Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                             Title: Differential signal Reference number: 155417; Naccession: 155417
                                                                                                                                                                                  Cross-references: EMBL:U07567; NID:g641963; Experimental source: Nb2-11C cell line
                                                                                                                                                                                                                                                                                                                                                     Residues: 1-412 <ALI>
                                                                                                                                                                                                                                                                                                                                                                                              Title: A prolactin-dependent immune cell Reference number: A41070; MUID:92041834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: mRNA; Residues: 1-610 <SHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:M74152; NID:g206389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shirota, M.; Banville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession:
                                                                                                                                                                                                                                                                                                        D'Neal, K.D.; Yu-Lee, L.Y.
Biol. Chem. 269, 26076-26082, 1994
                                                                                                                                                                                                                                                                                                                                                                  Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                   Accession: A41070
                                                                                                                                                                                                                                                                                                                                                                                                                               Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                               Chem.
 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP 19:
                             SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                                          SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNLTL-EVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSCRLAGLKPGTVYFVQVRCNPFGIYGSK 275
                                                                                                                                                                                                                   1-412 <RES>
                                                                                                                                                                     transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                              266, 20110-20117, 1991
                                                                                              Conservative
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                                                                                                           19.2%;
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                                                                                                                                                                                                                                                                          1 transduction of MUID:95014432
                                                                                            34;
                                                                                           Score 288.5;
Pred. No. 9.46
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S.; Jolicoeur,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 288.5; DB ;
Pred. No. 1.6e-18;
4; Mismatches 8(
                                                                                                                                                                                                                                                                                                                                                                                                             line
                                                                                                                                                                                                                                                                                                                                    PID: g206390
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                                                                                                           .4e-
                                                                                                                                                                                                 PID: g641964
                                                                                                                      DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                             expresses
                                                                                         Indels
                                                                                                                       Length
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                         A; Title: Purification and partial A; Reference number: A60380; MUID: 9
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                                                                                                 A; Molecule type: mRNA
A: Residues: 1-616 <EDE>
                                                                                                                               A; Reference number: A30304;
A; Accession: A30304
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A; Residues: 1-310 <BOU>
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Best Local
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protein
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C; Reywords: transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                        A;Cross-references: GB:M19304; NID:g206364; PID:g206365
                                                                                                                                                                                                                                         A;Reference number: A29884; MUID:88165059
A;Accession: A29884
                                                                                                                                                                                                                                                                                                                                                                                     Species: Rattus norvegicus (Norway rat)
Date: 30-Sep-1989 #sequence_revision 30
                                                                                                                                                                                                                                                                                       Title: Cloning and expression of the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 TOFKVFDLYPGOKYLVOTRCKPDHGYWSR 212
                                                                                                                                                                                                                                                                                                                    , J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, 69-77, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSCRLAGLKPGTVYFVQVRCNPFGIYGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNLTL-EVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQNGSSSSDPLYVDVTYIVEPEPP
                                                                           prolactin receptor #status predicted
                                                                                                                                                                                                                                                                                                                                                                                       30-Sep-1989 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275
                                                                                                                                                                                                                                                                                       prolactin receptor,
DB 2;
                                                                                                                                                                                                                                                                                                                                    J.; Edery,
Length
                                                                                AMAT'
                                                                                                                                                                                                                                                                                                                                    M.; Shirota,
                                                                                                                                                                                                                                                                                                                                                                                             20-Mar-1998
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Ва

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126 RNLTL-EVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ
                                                                                                                                                                                                             135 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP 191
                                                                                                                                                                     66 TTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP 125
                                                                                                                                                                                                                                                           15 SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                                                                                                   PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 246
                                                                                                                                                                                                                                                                                                 SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 134
                                        TSCRLAGLKPGTVYFVQVRCNPFGIYGSK
TOFKVFDLYPGQKYLVQTRCKPDHGYWSR
                                                                                                                                                                                                                                                                                                                                                                     19.2%;
                                                                                                                                                                                                                                                                                                                                                     34;
                                                                                                                                                                                                                                                                                                                                                                     Score 288.5;
Pred. No. 6.5
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  212
                                          275
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                                                                                   183
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A;Cross-references: GB:J04510; NID:g165669; PID:g165670 R;Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J. Int. J. Blochem. 22, 1089-1095, 1990
                                                                                                                                                                                                                                                                                                                                                                                                      prolactin receptor 2 precursor - rabbit
N;Alternate names: prolactin receptor, mammary gland
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #
                                                                                                                                                                                                                                                                                    C;Accession: A30304; A60380
R;Edery, M.; Jolicoeur, C.; Levi-Meyrueis, C.; Dusanter-Fourt, Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
A;Title: Identification and sequence analysis of a second form
artial sequence of the rabbit mammary gland prolactin MUID: 91146782
                                                                                                                                                                                                                                                         sequence analysis
MUID:89184578
                                                                                          ₩.J.;
                                                                                                                                                                                                                                                                                                                                                                                                             #text_change
                                                                                          wood,
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A; Title: Molecular cloning and characterization of the A; Reference number: A44257; MUID:93052397
A; Accession: A44257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: sequence extracted from NCBI backbone (NCBIP:118488)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ś
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interleukin-6 signal transducing molecule gpl30 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: the
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary; not compared with conceptual translation Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Rattus norvegicus (Norway rat)
Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Note: the amino end of the mature protein was blocked
;Reywords: blocked amino end; glycoproteil; transmembrane protein
;1-24/Domain: signal sequence #status predicted <SIG>
;25-616/Product: prolactin receptor 2 #status predicted <MAT>
;235-258/Domain: transmembrane #status predicted <TMM>
;59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                              237
                                                                                                  177 VLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPALKDELFQAKYQIRYRVEDSVD 236
                                                                                                                                                                   154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261
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                                                                                                                                                                                                                                                                                                               36 PVVQRGSNFTATCVLKEKCLQVYSVNATYIVWKTNHVAVPKEQVTVINRTASSVTFTDVV 95
                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                       WKVV---DDVSNQTSCRLAGLKPGTVYFVQVR 265
                                                                       PINFDPVDKVKPSPPHNLSVTNSEELSSILKLAWVNSGL--DSILKLKSDIQYRTKDAST 267
                                                                                                                                                                                          LHTNYSLKYKLRWYGQD-NTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSD 176
                                                                                                                                                                                                                                  FQNVQLTCNILSEGQIEQNVYGITILSGYPPDIPTNLSCIVNEGKNMLCQLDFGR--ETY 153
                                                                                                                                                                                                                                                                       GSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETF 117
                                                                                                                                                    LETNYTLKSE--WATEKFPDCRTKH--GTSSCMMGYTPIYFVNIEVWVEAENALGNVSSE
                                                                                                                                                                                                                                                                                                                                                       PTILIGSSLOATCSIHG---DTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPYLWVKWLPPTLVDVRSGWLTLQYEIRLKPEKAAEWE-THFAGQQTQFKILSLYPGQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSVRWVS--PPALKDF----LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVQVRCNP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHI-PKDLALFTPYEIWVEATURLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPGKPFIFKCRSPEKETFTCWWRPGADGG--LPTNYTLTYHKEGETITHECPDYKTGGPN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCYFSKKHTSIWTIYIITVNATNQMGSSVSDPRYVDVTYIVEPDPPVNLTL-EVKHPEDR
                                                                                                                                                                                                                                                                                                                                                                                                         79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -918 <WAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and characterization of the rat liver IL-6; MUID:93052397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 286; DB 2; 1
Pred. No. 2.7e-18;
26; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 281.5; DB 2; Length 918; Pred. No. 1.2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
299
                                                                                                                                                                                                                                                                                                                                                                                                     132;
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                                                                                    A; Molecule type: mRNA
A; Residues: 1-917 < RE2>
                                                                                                                                                                                                                                                            R;Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.
Immunol. 148, 4066-4071, 1992
A;Title: Molecular cloning of a murine IL-6
A;Reference number: 148370; MUID:92291532
A;Accession: 149699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted <MAT>
F;439-462/Domain: transmembrane #status predicted <TMM>
F;439-462/Domain: transmembrane #status predicted <TMM>
F;59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate
                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: DDBJ:D13154; NID:g222848; PID:d1002939; A;Experimental source: kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                         Species: Mus musculus (house mouse);Species: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 07-Feb-1997;Accession: I49699; I48370.
                                                                                                                                                         Accession: I48370
                                                                                                                                                                     Cross-references: GB:M83336; NID:g193591;
                                                                                                                                                                                             Residues: 1-917 <RES>
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Best Local
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Tanaka, M.; Maeda, K.; Okubo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 NSCYFDKKHTSFWTIYNITVRATNEMGSNSSDPHYVDVTYIVQPDPPVNVTLELKKPINR 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 HSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDV--HVSRVGGL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em. Biophys. Res. Commun. 188, 490-496,
le: Double antenna structure of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 YEVQVRCNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 KPYLVLTW-SPPPLADVRSGWLTLEYELRLKPEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 PPEKPTIIKCRSPEKETFTCWWKPGLDGG---HPTNYTLLYSKEGEEQVYECPDYRTAGP 286
                        gp130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGODNTCEEYHTVGP 145
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                                                                                                                                                                                                                                   translated from GB/EMBL/DDBJ
                                                                                                                          translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YIIQIHCKP 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDQLSVRWVSPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV 259
glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                          EMBL: x62646; NID: g840816;
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                                                                                                                                                                                                                                                                                                                                          M.; Taga, T.; Kishimoto,
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Pred. No. 1.1e-17;
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                                                                                                                                                                       PID:g193592
                                                                                                                                                                                                                                                                                             receptor-associated signal transducer,
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1992
                                                            PID: 9840817
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Query Match Best Local

Matches

78;

Conservative

6;

Mismatches

Similarity

18.5%;

Score 279; DB 2; Pred. No. 2e-17;

Length 917;

Indels

16;

Gaps

7

Db Db	B 8	g 8	B 8	g &
237 267	177 209	118 154	58 96	36
237 WKVVDDVSNQTSCRLAGLKPGTVYFVQVR 265	177 VLTLDVLDVYTTDPPPDVHVSRVGGLEDQLSVRWYSPPALKDFLFQAKYQIRYRVEDSVD 236 :	118 LHTNYSLKYKLRWYGQD-NTCEEYHTVGDHSCHIPKDLALFTPYEIWVEATNRLGSARSD 176	58 GSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETF 117 1 1 1 1 1 1 1 1 1	1 PTILIGSSLOATCSIHGDIPGATAEGLYWTLNGRRLDSELSRLLNTSTLALALANIN 57
	6 6	76	17	

Search completed: September 16, 1999, 20:42:1 Job time: 5403 sec

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein protein search, using sw model

Run on: September 17, 1999, 03:10:13; 3 ; Search time 35.09 Seconds (without alignments)
223.955 Million cell updates/sec

Title: Perfect score: Sequence: US-09-037-657-19 1505

PTLLIGSSLQATCSIHGDTP.....VYFVQVRCNPFGIYGSKKAG 278

Scoring table: BLOSUM62

77977 seqs, 28268293 residues

Database : SwissProt_37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	sus scrofa	975		CHK_FIG	٠,	200	9 6	1	27
	rattus norv.	1777		1000	ر د	200		1	26
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	١.	0888		HUMA	_	468	10.5	158.5	23
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	homo sa	P26992		CNTR_HUMAN	_ د	2/1	1 1	•	10
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	melead?	091094		PRLR_MELGA	ш	831	œ	280	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oddified and this statement notities requires a license
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1990 (REL.
01-AUG-1990 (REL.
15-DEC-1998 (REL.
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12-AUG-1990 (REL. 15, LAST ESQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ROLACTIN RECEPTOR PRECURSOR (PRL-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LI S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       he European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OMERS W., ULTSCH M., DE VOS A.M., KOSSIAKOFF A.A.;
The X-ray structure of a growth hormone-prolactin receptor complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LI S., GOULD D., DJIANE J., KELLY P.A.;
Identification of a CDNA encoding a long form of prolactin receptor human hepatoma and breast cancer cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A40144; A40144
                                                                                                                                                                                                                                                                                                                                                                                   PS00241; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATARRHINI;
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                                                                                                 69505 MW;
                 20.5%;
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; Score 308.5; DB 1; ; Pred. No. 3.5e-20; 27; M1smatches 85;
                                                                                       BY SIMILARITY.
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6924E155 CRC32;
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                       POTENTIAL.
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Q90374;
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01-NOV-1997 (REL. 35
15-JUL-1998 (REL. 36
PROLACTIN RECEPTOR I
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DOMAIN
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                                                                                                                                                    MAIN
                                                                                                                                                                                                                                                                          ROSITE;
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                                                                                                                                                                   RANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90374;
1-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                    and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                       PS00241; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HORSEMAN N.D.;
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                                                                                                                                                                                                                            TRANSMEMBRANE;
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METAZOA; CHORDATA; VERTEBRATA;
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BELONGS TO THE CYTOKINE FAMILY OF REC
CONTAINS 4 FIBRONECTIN TYPE III-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35, CREATED)
35, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDAT
PRECURSOR (PRL-R)
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439
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           POTENTIAL.
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FXTRACELLULAR (POTENTIAL).
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BY SIMILARITY.
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008501; 062099; p15213; p15212;

01-APR-1990 (REL. 14. CDEPART)
DAVIS J.A., LINZER D.I.H.; 
"Expression of multiple fo 
liver.";
                         SEQUENCE FROM N.A. (FOUNT OF THE STRAIN-SWISS WEBSTER;
MEDLINE; 89261824.
                                                                   SEQUENCE FROM N.A. (FORM PRL-R3).
STRAIN-BALB/C; TISSUE-MAMMARY GLAND;
EDBRY M., PEZET A., NANDI S., KELLY P.A.;
SUBMITTED (JUN-1993) TO EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                                                                                                                                               MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
MURIDAE; MURIDAE; MURINAE;
                                                                                                                        SUBMITTED
                                                                                                                                   SASAKI
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              "Cloning and sequencing of the long-form prolactin receptor."; SENE 134:263-265(1993)
                                                                                                                                                                                                                                                                                                                                                                          PROLACTIN RECEPTOR PRECURSOR (PRL-R)
                                                                                                                                                                              Changes in prolactin
                                                                                                                                                                                                        MEDLINE; 93307149
                                                                                                                                                                                                                                                                                          (EDLINE;
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                                                                                                                                  EQUENCE FROM N.A. ASAKI M.;
                                                                                                                                                                                                                  RAIN-SWISS WEBSTER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPEKPTIIKCRSPEKETFTCWWKPGSDGG---HPTNYTLLYSKEGEERVYECPDYKTAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPYLVLTW-SPPPLADVRSGWLTLDYELRLKPEEAEEWETI-FVGQQTHYKMFSLNPGKK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDQLSVRWVSPPALKDF - - - LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                       94085788
                                                                                                                       (JUL-1992)
                                                                                                                                                                                                                                                                                                                                                                                (REL. 14, CREATED)
(REL. 31, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
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                                                                                                                                                               133:224-232(1993).
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336
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                                      (FORMS PRL-R2 AND R; TISSUE-LIVER;
                                                                                                                                            (FORM PRL-R3)
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R; TISSUE=LIVER;
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                                                                                                                                                                                   receptor expression
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FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: THREE FORMS, PRL-R7, PRL-R2 AND PRL-R3
                                                            ALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI
                                                                                                                           WKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP
                                                                                                                                                                                    FTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVS--PP 214
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L14811; G293770; -.
D10214; G220576; -.
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PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG
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Pred. No. 1.3e-18;
7; Mismatches 85;
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L -> F (IN REF. 2).
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PTTEFLCDL (IN PRL-R1).
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                                                                            CHAIN
                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                 PFAM; PF00041;
                                                                                                                                        PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
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01-FEB-1995 (REL.
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INTERLEUKIN-6 RECE
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PRIMATES; CATARRHINI;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
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HIBI M., MURAKAMI M.,
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                                                                                                                                                                                                                                                                                                                                                                                                 ONE IG-LIKE DOMAIN
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                                                                                                           TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
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REL. 31, LAST SEQUENCE UPDATE)
REL. 37, LAST ANDOTATION UPDATE)
RECEPTOR BETA CHAIN PRECURSOR (IL-(
SDUCER) (MEMBRANE GLYCOPROTEIN 130)
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POTENTIAL.

CYTOPLASMIC (POTENTIAL)

IG-LIKE C2-TYPE DOMAIN.

FIBRONECTIN TYPE-III.
                                                     INTERLEUKIN-6 RECEPTOR BETA CHAIN EXTRACELLULAR (POTENTIAL).
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  receptor cDNA spe
BIOCHEM. BIOPHYS.
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EDERY M., DJIANE J., KELLY F
"Expression of two forms of
                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1988 (REL. 09, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PROLACTIN RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAT
                                                                             STRAIN-SPRAGUE-DAWLEY; MEDLINE; 90241201.
                                                                                                                                                                                                                                                                                                                                       EUKARYOTA;
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EUKARYOTA; METAZOA; CHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P05710;
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                                           Isolation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 LHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDV
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                                                                                                                  EQUENCE FROM N.A.
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77; Conserv
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                                                           BUCZKO
                                    BUCZKO E., TSAI-MORRIS C.H.,
and characterization of two
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RES. COMMUN.
                                                                                                                  (LONG FORM AND SHORT
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                                                                                                                                                                                                                   D., ALI S., JOLICOEUR C., KELLY P.A.;
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                                                                                                TISSUE-OVARY;
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                                                                                                                                                                                            prolactin
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Pred. No. 2.6e-18;
7; Mismatches 13;
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168:415-422(1990).
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                                    HU Z.Z.,
novel rat
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                                    z., DUFAU M.L.;
rat ovarian la
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                                  lactogen
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EMBL; M57668; EMBL; M34083; EMBL; L48060; EMBL; U34730; EMBL; M19304; EMBL; M74152; EMBL; U07567; U07567;
                      DOMAIN
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DISULFID
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CARBOHYD
CARBOHYD
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DOMAIN
DOMAIN
           VARSPLIC
                                                                                                              DOMAIN
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between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Differential signal transduction
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SHIROTA M., BANVILLE D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED
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                                                                                                                                 SIGNAL
                                                                                                                                                            PFAM; PF00041;
HSSP; P16471;
                                                                                                                                                                                                                                                                                                        modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                             prolactin receptors. Activation cell proliferation. ":
                                                                                                                                          ALTERNATIVE
                                                                                                                                                                                                                                                                                               or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prolactin-dependent prolactin receptor.
                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED
SPLICING OF THE PRLR GENE.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEE
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DO
                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferation
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                                                                                                                                                    TRANSMEMBRANE;
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                                                                                                                                                                                                                                                                                               email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M., JOLICOBUR C., OKAMURA H., GAGNON J., EDERY M.,
BANVILLE D., DUSANTER-FOURT I., DJIANE J., KELLY P.A.;
and expression of the rat prolactin receptor, a member of
hormone/prolactin receptor gene family.";
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RECEPTOR_CYTOKINES_2;
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R., MURTHY K.K., BOIE
) TO EMBL/GENBANK/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                        A RECEPTOR
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                                                                                                                                                  GLYCOPROTEIN; SIGNAL; REPEAT;
                                                                POTENTIAL.

PROLACTIN RECEPTOR.

EXTRACELLULAR (BY SIMILARITY).

BY SIMILARITY.

CYTOPLASMIC (BY SIMILARITY).

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.
POTENTIAL.
EVKQLKDKKTYLWVKWSPPT
KLN (IN SHORT FORM).
                                                 BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                  removed
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DATA BANKS.
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Best Local Similarity
Matches 76; Conserv
                                                                           PROTEINS 27:459-468(1997).
                                                                                                                                                                              receptor by molecular cloning mammary gland.";
PROC. NATL. ACAD. SCI. U.S.A.
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CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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01-APR-1990
01-APR-1990
15-JUL-1998
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VARSPLIC
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IEDLINE; 89184578.
                                                                                                                  ALABY D., THOREAU Homology modeling
                                                                                                                                                                                                                                    ETRIDOU B.,
                                                                                                                                                                                                   DERY M., JOLICOBUR C., LEVI-MEYRUBIS C., DUSANTER-FOURT ETRIDOU B., BOUTIN J.M., LESUBUR L., KELLY P.A., DJIANE Identification and sequence analysis of a second form of eceptor by molecular cloning of complementary DNA from I
                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
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                      SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
       SWISS-PROT
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                                                                                                                                             97248733
                                                                                                                                                                                                                                                                                      JS CUNICULUS (Kh...
"ETAZOA; CHORDATA; VEA...
"TAE; ORYCTOLAGUS.
                                                                                                                                                                                                                                                                                                                                                                        (REL. 14, CREATED)
(REL. 14, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
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KGKSEELLSALGCODFPPTSDCEDLIVEFL ->
TGSPSKKVDLYLALPGGFOKLDNAGELDY (I
MEDIUM FORM).

MISSING (IN MEDIUM FORM).

MISSING (IN FORM NB2).

V -> A (IN REF. 2).

V -> A (IN REF. 2).

G -> V (IN REF. 2).

E -> K (IN REF. 2).

A -> G (IN REF. 2).

A -> G (IN REF. 2).
                                                                                                                  prolactin
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Pred. No. 2.1e
34; Mismatches
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                                                                           FOR THE ANTERIOR
                                                                                                                MORNON J.P.;
actin hormone
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 is produced through a
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                                                                           PITUITARY HORMONE
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collaboration
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Best Local Similarity
                                                                                                                                                                                                                                                                                                       P40190;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (
INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (
                                                    "Molecular cloning and charact transducing molecule, gp130."; GENOMICS 14:666-672(1992).
                                                                                                                 TISSUE-LIVER;
MEDLINE; 93052397.
WANG Y., NESBITT J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                IL6B_RAT P40190;
                                                                                                                                                                                        SEQUENCE FROM N.A.
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DISULFID
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                                                                                                                                                                                                                                                        RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHOR
                                                                                                                                                                                                                                  RODENTIA; SCIUROGNATHI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 KPYLWYKWLPPTLYDYRSGWLTLQYEIRLKPEKAAEWE-THFAGQQTQFKILSLYPGQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 SCHI-PKDLALFTPYEIWYEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQ 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 FYQVRCNP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 LSVRWVS--PPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVY
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PFAM; PF00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 SCYPSKKHTSIWTIYITVNATNQMGSSV5DPRYVDVTXIVEPDPPVNLTL-EVKHPEDR
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FUNCTION: SIGNAL TRANSDUCING MOLECULE. THE RECEPTOR STIL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPGKPFIFKCRSPEKETFTCWWRPGADGG--LPTNYTLTYHKEGETITHECPDYKTGGPN 84
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AE; MURINAE;
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Pred. No. 3.6e-18;
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BY SIMILARITY.
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                                                                                                                                                                                                                              MAMMALIA;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A44257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M92340; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. entities requires a license agreement (See
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177 VLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute.
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SIMILARITY: COUNTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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                                                              LHTNYSLKYKLRWYGQD-NTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSD
                                                                                              FONVOLTCNILSEGOIEONVYGITILSGYPPDIPTNLSCIVNEGKNMLCOLDPGR--ETY
                                                                                                                              GSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETF
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                                 LETNYTLKSE--WATEKFPDCRTKH--GTSSCMMGYTPIYFYNIEVWVEAENALGNVSSE
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29.0%;
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                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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; Mismatches
                                                                                                                                                                                                                                            Score 281.5;
Pred. No. 1.
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; E6EDFCD0
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PROSITE; PS00241; RECEPTOR_CYTOKINES_1;

PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                               CARBOHYD
                                                                                                                                                                                                                                                PFAM; PF00041; fn3; 4. HSSP; P16471; 1BP3.
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EUKARYOTA; MET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-WHITE LEGHORN; TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994
                                                                                                                                      MAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EOGNATHAE;
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                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WKVV----DDVSNQTSCRLAGLKPGTVYFVQVR 265
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METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA;
: GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALL
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(REL.
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29, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDAT
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of chicken prolactin receptor deduced
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POTENTIAL.
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POTENTIAL.
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                                                                                                                                     FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                                                                     CYTOPLASMIC FIBRONECTIN
                                                                                                                                                                                         POTENTIAL.
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OR FOR THE ANTERIOR
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                                                                                                                                                                                                                                     SIGNAL; REPEAT
     CRC32;
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Matches
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TRANSMEM
                                                                                                                                                                                                                                                    EMBL; L76587;
EMBL; U22947;
EMBL; U22924;
                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   091094; Q91091; Q91092;
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                      DOMAIN
                                                                                                                                                                                                           PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
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                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration oetween the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PITTS G.R., YOU S.K., FOSTER D.N., SUBMITTED (MAR-1995) TO EMBL/GENBAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZHOU J.F., ZADWORNY D.,
SUBMITTED (JUN-1996) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MELEAGRIS GALLOPAVO (COMMON TURKEY).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA;
NEOGNATHAE; GALLIFORMES; MELEAGRIDIDAE; MELEAGRIS.
                                                                                                                                                                                              FAM; PF00041; fn3; 4.
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ZHOU J.F., ZAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                             ECEPTOR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP 145
                                                                                                                                                       TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL;
                                                                                                                                                                                                                                                     G973166;
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122
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428
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5) TO EMBL/GENBANK/DDBJ DATA BANKS.
IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
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EMBL/GENBANK/DDBJ DATA BANKS.
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                                                                                                PROLACTIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                             FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                 CYTOPLASMIC
FIBRONECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.5e-17;
7; Mismatches 82;
                                                                                     POTENTIAL.
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              TYPE-III
                                                                  (POTENTIAL).
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Best Local
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                                                                                        -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THE SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TEXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995
01-FEB-1995
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                        MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
SEQUENCE
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                                                                                                                                                                                              SATTO M., YOSHIDA K., HIBI M., TAGA T., KISHIMOTO T.;

"MOLECULAR CLORING of a murine IL-6 receptor-associated signal transducer, gpl30, and its regulated expression in vivo.";

J. IMMUNOL. 148:4066-4071(1992).

-I- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6. LIF. OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATIN SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES.

AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE PROPERTY OF THE SIGNAL.
                                                                                                                                                                                                                                                                                                                                   SAITO M., YOSHIDA K., HIBI M.,
                                                                                                                                                                                                                                                                                                                                                    STRAIN-ICR; TISSUE-MACROPHAGE; MEDLINE; 92291532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L6B_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 PPEKPTITKCRSPEKETFTCWWKPGLDGG---HPTNYTLLYSKEGEEQVYECPDYRTAGP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP 145
DEVELOPMENTAL STAGE: IN EMBRYONIC 6 OF GESTATION. IT REACHES A PEAK DURING THE REST OF EMBRYOGENESIS. SIMILARITY: BELONGS TO THE IMMUNOC ONE IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEB-1995 (REL. 31, CREATED)
FEB-1995 (REL: 31, LAST SEQUENCE UPDATE)
DEC-1996 (REL. 37, LAST ANIOTATION UPDATE)
ERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
IGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
                                                                                                                                                                                   EMBRYONIC DEVELOPMENT
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69; Conserv
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Pred. No. 1.8e-17;
5; Mismatches 83
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ON DAY 8 AND GRADUALLY DECLINES
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IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

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Best Local Similarity
Matches 78; Conser
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EMBL; M83336; G193592; -.
MGD; MGI:96560; IL6ST.
PROSITE; PS00340; RECEPTOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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European Bioinformatics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                  GSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETF 117
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                                                                                                                                                    WKVV---DDVSNQTSCRLAGLKPGTVYFVQVR 265
                                                                                                                                                                                           SINFDPVDKVKPTPPYNLSVTNSEELSSILKLSWVSSGL--GGLLDLKSDIQYRTKDAST
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    STANDARD;
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28.7%;
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Pred. No. 2.5e-17;
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    PRT;
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      8
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; CERVOIDEA; CERVIDAE; CERVINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROLACTIN RECEPTOR PRECURSOR (PRL-R).
                                                                                                         CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLARKE I.A., EDERY M., LOUDON A.S., RANDALL V.A., KELLY P.A., JABBOUR H.N.;
"Expression of the prolactin receptor gene during non-breeding seasons in red deer (Cervus elaphus): expression of two forms in the testis.";
J. ENDOCRINOL. 146:313-331(1995).
-I- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00041; fn3; 2. HSSP; P14787; 1AN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X94953; E218406; -
PROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1.
PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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between the Swiss Institute of Bioinformatics and the EMBL
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-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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POTENTIAL.
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'721F0366 CRC32;
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TSCRLAGLKPGTVYFVQVRCNPFGIYGSK
                                                                                                                           QDNTCEEYHTVGPHSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP 191
                                           ANLTL-ELKHPEDRKPYLWIKWFPPTLTDVKSGWFMIQYEIRLKPETAADWE-IHFAAKQ
                                                                     PDVHVSRVGGLEDQLSVRWVS--PPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ
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Pred. No. 2.4e
)5; Mismatches
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BOVIN PRLR_BOVIN Q28172;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institu modified and this statement entities requires a license
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-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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SCOTT P., KESSLER M.A., SC
Molecular cloning of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOS TAURUS (BOVINE).
EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ERTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE;
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01-NOV-1997 (REL. 35,
15-JUL-1998 (REL. 36,
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                               YEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWV--SPPALK
                                                                                                MKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHI-PKDLALFTP 159
                                                                                                                                                                 SRILNTSTLALALANINGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRN 100
YVITVNAINOMGISSSDPLYVHVTYIVEPEPPANLTL-ELKHPEDRKPYLWIKWSPPTMT 157
                                                                                                                                          SRVVFILLIFLSVSLLNG---QS------
                                                                                                                                                                                                                           Similarity
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ON: THIS IS A RECEPTOR
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35, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
PRECURSOR (PRL-R).
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                                                                                                                                                                                                           37;
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                                                                                                                                                                                                                         Score 276;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                            POTENTIAL.
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                      88; Indels
                                                                                                                                                                                                                                      Length 581;
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Matches 64; Conserv
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SEQUENCE
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use by non-profit institutions as 1
modified and this statement is not rem
                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SANDRA O., SOHM F., DE LUZE A., PRUNET P., EDERY M., KELLY P.A.; "Expression cloning of a cDNA encoding a fish prolactin receptor."; PROC. NATL. ACAD. SCI. U.S.A. 92:6037-6041(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA;
TELEOSTEI;
                                                                                                                                                                           PRANSMEM
                                                                                                                                                                                                                                                                                         EMBL; L34783; G903847;
                                                                                                                                                                                                                                                                                                                                                                                                              1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95320210.
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215 WSE 217
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      Conservative .
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35, LAST SEQUENCE UP
36, LAST ANNOTATION
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              15.5%;
                                                                   WW;
                                                                                                                                                                                                                     GLYCOPROTEIN; SIGNAL;
  Score 233; DB 1; Pred. No. 2.1e-13; 25; Mismatches 85;
                                                                               POTENTIAL.
                                                                                                                                            CYTOPLASMIC FIBRONECTIN
                                                                                                       BY SIMILARITY.
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01-FEB-1995 (REL. 3)
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GRANULOCYTE COLONY 9
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HOMO SAPIENS (HUMAN).
HOMO SAPIENS (HUMAN).
HOMO SAPIENS (HUMAN).
LARSEN A., DAVIS T., CURTIS B.M., G
PARK L., SORENSEN E., MARCH C.J., S
"A CDNA clone expressed in natural
encodes a secreted protein.";
J. EXP. MED. 172:1559-1570(1990).
                                                                                                               YAMASAKI K., NAITO S., ANAGUCHI H., OHKUBO T., "Solution structure of an extracellular domain motif of the granulocyte colony-stimulating facinteraction with ligand.";
NAT. STRUCT. BIOL. 4:498-503(1997).
                                                                                                                                                                                                                                                                                                                                                                                  factor receptor.";
PROC. NATL. ACAD. SCI. U.S.A.
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MEDLINE; 91011257.
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                                                                                                                                                                                                                                                                                                            stimulating
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                                                                                                                                                                                       STRUCTURE BY NMR OF 227-334.
                                                                                                                                                                                                                          receptor.
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                                                                                                                                                                                                                                                                          DOMAINS STRUCTURE.
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                                                                               MEDLINE;
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                                                                                          D-STRUCTURE MODELLING OF 125-331.
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148:259-266(1992).
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31, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDAT
Y STIMULATING FACTOR RECEP
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                                                                                                                                                 OTA Y.;
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                                                       granulocyte
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                                          and mutagenesis.";
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                                                                                                                                       receptor
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SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOM SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPT DATABASE: NAME-PROW; NOTE-CD guide CD114 entry; WWW-"http://www.ncb1.nlm.n1h.gov/prow/cd/cd114.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF THE RECEPTOR.
TISSUE SPECIFICITY: ONE OR
                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-98
                                                                                                                                                                                                                                                                                                                                                                                                           A38252
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EVENTS AT THE CELL SURFACE.

-I- SUBURIT: DIMER (PROBABLE).

-I- SUBURILULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM,
WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM

TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES. THE GGSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE GSCFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.

ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS, GCSFR-1 (SHOWN UNDER),

GCSFR-2, GCSFR-3 AND GCSFR-4/D7, ARE PROBABLY PRODUCED ALTERNATIVE SPLICING OF THE SAME GENE. THEY DIFFER IN : THEIR ВХ ç

TERMINAL PORTION.

DISEASE: DEFECTS IN CSF3R ARE A CAUSE OF KOSTMANN SYNDROME.

ALSO KNOWN AS SEVERE CONGENITAL NEUTROPENIA (SCN).

IMMUNOGLOBULIN SUPERFAMILY. CONTAINS

DOMAINS

RECEPTORS

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EPEAT; ALTERNATIVE SPLICING; X55721; G31697; -: X55720; G31699; -. ; S71484; G240884; -. ; M59818; G183047; -. PS00341; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; POTENTIAL.
POTENTIAL.
POTENTIAL. POTENTIAL.
POTENTIAL.
POTENTIAL. POTENTIAL.
POTENTIAL.
VLYGOLLGSPTSPGPGHYLRCDSTOPLLAGLTPS
AGPPRRSAYFKDQIMLHPAPPNGLLCLFPITSVL FIBRONECTIN BY SIMILARIT CYTOPLASMIC (POTENTIAL) GRANULOCYTE IG-LIKE C2-TYPE DOMAIN. FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III FIBRONECTIN EXTRACELLULAR (POTENTIAL) 3D-STRUCTURE FIBRONECTIN SIMILARITY. TYPE-III. TYPE-III COLONY STIMULATING FACTOR SIGNAL; ţ

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NAT. STRUCT. BIOL. 4:498-504(1997).

-I- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-
ADDITION IT MAY FUNCTION IN SOME ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                    P40223;
01-FEB-1995 (REL. 3
01-FEB-1995 (REL. 3
15-JUL-1998 (REL. 3
GRANULOCYTE COLONY
                                                                                                                                                                      stimulating
                                                                                                                                                                                                                                      MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
EUKARYOTA: COTHROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 90235283. FUKUNAGA R., ISHIZ.
                                                                                                                               STRUCTURE BY NMR OF 225-333.
                                                                                                                                                          CELL 61:341-350(1990).
                                                                                                                                                                                                                                                                                        CSF3R OR CSFGR
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     SUBUNIT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSPEAAPPQAGCLQ----LCW--EPWQPGLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GETFLHTNYSLK-YKLRWYGO---DNTCEEYHTVGPHSCHIP-KDLALFTPYEIWVEATN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSRQQSGDNLVCHARDGS---ILAGSCLYVGLPPEKPFNISC-WSRNMKDLTCRWTPGAH 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLGSARSDYLTLDVLDVV-----TTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -ETHLPTSFTLKSFKSRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLYQNMGIWVQAEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIVHLGDPITASCIIKQNCSHLDPEPQILWRLGAELQPGGRQQRLSDGTQESIITLPHLN
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DIMER (PROBABLE)
                                                                                                                                                                              ISHIZAKA-IKEDA E., SETO Y., NAGATA S., cloning of a receptor for murine granul
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31, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
36, LAST ANNOTATION RECEPTOR PRECURSOR (G-CSF-R).
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                     GRANULOCYTE COLONY-STIMULATING FACTOR.
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Pred. No. 2.
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MISSING (IN GCSI
E -> ELPGPRQGQWI
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PDPAHSSLGSWVPTIMEEDAFQLPGLGTPPITKLTVLEEDE
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.9e-12;
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                                                                       in containing the WSxWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M58288; G193455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch
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                                                                                     94
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                 GSARSDVLTLDVLDVVTTDPP------PDVHVSRVGGLEDQLSVRWVS-PPALKDFLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: FO
SIMILARITY: BELONGS TO
ONE IG-LIKE DOMAIN.
GSSESPKLCLDPMDVVKLEPPMLQALDIGPDVVSHQPGCL--
                                    THLPTSFILKSFRSRADCOYQGDTIPDCVAKKRONNCSIPRKNLLLYQYMAIWVQAENML
                                                         TFLHTNYSLK-YKLR---WYGODNTCEEYHTVGPHSCHIP-KDLALFTPYEIWVEATNRL
                                                                                                  NGSROOSGDNLYCHARDGSILAGSCLYYGLPPEKPFNISCWSR-NMKDLTCRWTPGAHGE 115
                                                                                                                                           PTILIGSSLOATCSIHGDTPGATAEG-LYWTLNGRRL-PSELSRLL--NTSTLALALANL
                                                                               NYT-QAFLFCLVPWEDSVQLLDQAELHAGYPPASPSNLSCLMHLTTNSLVCQWEPGP--E
                                                                                                                       PVVRLGDPVLASCTISPNCSKLDQQAKILWRLQDEPIQPGDRQHHLPDGTQESLITLPHL
                                                                                                                                                                       83;
                                                                                                                                                                                 Similarity
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28.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE
                                                                                                                                                                    46;
                                                                                                                                                                   Score 221.5;
Pred. No. 3.26
6; Mismatches
                                                                                                                                                                                                                       POTENTIAL.
D55F84D4
                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                POTENTIAL.
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                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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BY SIMILARITY.
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FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                   FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                             FIBRONECTIN TYPE-III
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                       IG-LIKE C2-TYPE DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                YTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMUNOGLOBULIN
                                                                                                                                                                                                                       CRC32;
                                                                                                                                                                            .2e-12;
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                                                                                                                                                                   Indels
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                                                                                                                                                                   31;
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Search	당.	Ş
2	264	222
noleted:	EQECELR	QAKYQIR
Search completed: September 17, 1999, 03:10:14	264 EQECELRYQPQLKGANWTLVFHLPSSKDQFELCGLHQAPVYTLQMRC 310	222 QAKYQIRYRVE-DSVDWKVVDDV-SNQTSCRLAGLKPGTVYFVQVRC 266
r 17.	MILVE	- WKVVI
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) <u> </u>	 GLHQAP	GLKPGT
	 VYTLQMRC	VYFVQVRC
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Perfect score:
Sequence:
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                                                                                   178
172.5
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1505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_organelle:*
sp_phage:*
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sp_unclassified:*
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p_invertebrate:*
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060468 homo sapien
060469 homo sapien
092920 homo sapien
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092921 homo sapien
013593 homo sapien
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046386 mustela vis
P79203 ovis aries
099665 homo sapien
016542 homo sapien
088507 mus musculu
P97378 mus musculu
P97378 mus musculu
057520 xenopus lae
002671 sus scrofa
                                                                                                                                                                                                                                              046561 ovis aries
018880 bos taurus
093404 oreochromis
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057519 xenopus lae
Q16354 homo sapien
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278 325	168 NYSLKYKLRWYGODNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEAINRLGSARSDVLTL 227 181 DVLDVYTTDPPPDVHVSRVGGLEDGLSVRWYSPPALKDFLFQAKYQIRYRVEDSVDWKVV 240 [:	AGSCLYVGLPPEKPENISCWSRNMKDLICRWIP AGSCLYVGLPPEKPVNISCWSKNMKDLICRWIP 	LIGSSLQATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALAN 	ry Match 97.2%; Score 1463; DB 4; Length 422; t Local Similarity 96.4%; Pred. No. 2.6e-135; ches 268; Conservative 5; Mismatches 5; Indels 0. Gans of	30 142 9.4 279 11 Q64236 31 134 8.9 229 4 O75269 32 134 8.9 229 4 O75269 33 134 8.9 229 4 O75269 34 132.5 8.8 971 11 O36600 35 132.5 8.8 971 11 O35265 36 129.5 8.6 316 11 O35265 37 128.5 8.6 316 11 O35265 38 129.5 8.6 316 11 O35265 38 129.5 8.6 316 11 O35265 39 128.5 8.6 316 11 O35265 40 123 8.2 229 4 O24233 40 123 8.2 229 6 O27950 42 123 8.2 229 6 O27950 43 120.5 8.0 1093 11 O70535 44 120.5 8.0 1093 11 O70535 45 120.5 8.0 1277 13 O98802 46 120.5 8.0 1277 13 O98802 47 120.5 8.0 1277 13 O98802 48 120.5 8.0 1277 13 O98802 49 O1-NOV-1998 (TERMELTEL 108, Created) O1-NOV-1998 (TERMELTEL 108, Created) O1-NOV-1998 (TERMELTEL 108, Created) O1-NOV-1998 (TERMELTEL 108, Created) O1-NOV-1998 (TERMELTEL 108, Last sequence update) O1-NOV-1998 (TERMELTEL 108, Created) O1-NOV-1998 (TERMELTEL 1

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RESULT OF THE PROPERTY OF THE 
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Best Local
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01-JUN-1998
01-JUN-1998
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-NOV-1998 (TIEMBLIEL 08, Last annotation updat
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Submitted (JAN-1998) to the EM
EMBL; AF041845; AAAC03531.1; -.
PFAM; PF00041; fn3; 4
SEQUENCE 881 AA; 99003 MW;
                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          016354;
                                                                                                                                                                                                                                                                                                                                                                              PROLACTIN RECEPTOR (FRAGMENT)
                                                                                                                             cancer cell lines."
                                                                                                                                                                                     TUH G., WELLS J.A.;
                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 95286597.
                                                                                                                                                                                                                                                                                               Sutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa
Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kenopus laevis (African clawed frog).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 VDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRC
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                                                                                                                                                    Prolactin receptor antagonists that inhibit the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
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                                                                                                          Biol.
                           LIER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLSH--RWAHFGANYCRGANNSC-----TIHSP-GFQFYIDTTFQVEATNELGIQK
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                                         ol. Chem. 270:13133-1
$78505; AAB34470.1;
PF00041; fn3; 2.
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206
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                                                                                                 270:13133-13137(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGSROO
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                                                                                                                                                                                                                                                                                       Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                      Chordata; Craniata;
23950 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.7%;
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Pred. No. 1
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D7E57266 CRC32;
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                                                                                                                                                                                                                                                                                                                   Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
..5e-23;
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Query Match Best Local :

Similarity

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Score 302; Pred. No. 4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 98001468. BIGNON C., BINART
                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                      BIGNON C., DJIANE J.
Submitted (JAN-1998)
EMBL; AF041257; AAB9
                                                                                                                                                                                                                                                                                                                                                                                                             "Long and short forms of the owine prolactin receptor: cDNA cloning and genomic analysis reveal that the two forms arise by different alternative splicing mechanisms in ruminants and in rodents.";

J. Mol. Endocrinol. 19:109-120(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         046561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      046561
                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                           PFAM; PF00041; fn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROLACTIN RECEPTOR LONG
                             133
                                                                                                  249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 YLVQVRCKP
                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 YFVQVRCNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 QLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 HSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLED
                                                                                   73
                                                                                                                                           20
                                                                                                                                                                  75 SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 134
                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
CRLAGLKPGTVYFVQVRCNPFGIYGSK 275
                        LTL-ELKHPEDRKPYLWIKWSPPTLTDVKSGWFSIQYEIRLKPEKATDWE-THFAPKLTQ
                                                      VHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTS
                                                                                HECPDYKTGGPNSCYFSKKYTSIWKMYVITVSAINOMGISSSDPLYVDVTYIVEPEPPVN
                                                                                                                                        SLLNGQS-----PPEKPKLIKCRSPGKETFTCWWEPGADGG--LPTNYTLTYRKEGETLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE-IHFAGQQTEFKILSLHPGQK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLELAV-EVKQPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTYHREGETLMHECPDYITGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74;
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                   1
25
581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cetartiodactyla;
                                                                                                                                                                                               Conservative
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581
65235 >
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06, Last sequence update)
10, Last annotation updat
FORM PRECURSOR.
                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                   POTENTIAL.
PROLACTIN R
6792A7C7
                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                             Score 282.5;
Pred. No. 1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHULER L.A., KELLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   581
                                                                                                                                                                                                                                                                    RECEPTOR :7 CRC32;
                                                                                                                                                                                                             .6e-19;
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                                                                                                                                                                                                                           BB
                                                                                                                                                                                               87;
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                                                                                                                                                                                                                           6.
                                                                                                                                                                                                                                                                                  LONG
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                           581;
                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                             Gaps
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                          190
                                                      248
                                                                                                                                        72
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                                                                                132
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Best Local
                            "EXPIRAISHI K., MATSUDA M., MORI T., TETSUYA H.;
"Expression of prolactin and cortisol receptor gene in stages of tilapia (Oreochromis mossambleus).";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF080247; AAC31825.1;
PEAM, PF00041; fn3; 2.
                                                                                                                                                                               Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Actinopterygi
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha
Perciformes; Labroidei; Cichlidae; Tilapia.
                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAY-1999 (TrEMBLrel. 10, Last annotation updat
                                                                                                                                                                                                                                                               PROLACTIN RECEPTOR (FRAGMENT)
                                                                                                                                                              EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               -NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                            215 WSE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 DVKSGWFIIQ--YEIRLKPEKATDWE-THFTLKQTQLKIFNLYPGQKYLVQIRCKPDHGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 YEIWVEATNRLGSARSDYLTLDYLDVYTTDPPPDVHVSRYGGLEDQLSVRWV--SPPALK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 MKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHI-PKDLALFTP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 YVITVNAINOMGISSSDPLYVHVTYIVEPEPPANLTL-ELKHPEDRKPYLMIKWSPPTMT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 KETFTCWWEDGADGG--LPTNYTLTYHKEGETLIHECPDYKTGGDNSCYFSKKHTSIWKM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROLACTIN RECEPTOR SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 SRLLNTSTLALALANLNGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ddocrinology 138:3187-3194(1997).

IBL; AF027403; AAB8399.1; -.

'AM; PF00041; fn3; 2.99.1; -.

CUENCE 296 AA; 33854 MW; 8B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
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|-JAN-1998 (TIEMBLIEL 05, Last sequence update)
|-NOV-1998 (TIEMBLIEL 08, Last annotation update)
|| OLACTIN RECEPTOR SHORT FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-----FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIY 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L.A., NAGEL R.J., GAO J.,
tin receptor heterogeneity
        346
346 AA;
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                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
346
; 39203 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33854 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 276; DB 6;
Pred. No. 2.8e-19;
 1E8A63B9 CRC32
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                                                                                                                                                                                                                                                                                                                                              346 AA.
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                                                                                                                                                                                                                                                                        update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KESSLER M.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and maternal
                                                                                                                                                                                                 Percomorpha;
                                                                                               early-life
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            01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAY-1999 (TrEMBLrel. 10,
                                                         046386;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                   189
                                                                                                                                                                                                                                                                                                                                                                                                JABBOUR H.N.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y14753; CAA75048.1;
PFAM; PF00041; fn3; 1.
                                                                                                                                                      247 TSCR 250
                                                                                                                                                                   131 ANLTL-ELKHPEDRKPYLWIKWEPPTLTDVKSGWFMIQYEIRLKPETATDWE-HDDLHPP 188
                                                                                                                                                                                                            192
                                                                                                                                                                                                                                            133 QDNTCEEYHTVGPHSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVVTTDPP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cervus elaphus nelsoni (American elk).
Eukaryota; Metazoa; Chordata; Craniata
Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            73 DGSILAGSCLYVGLPPEKPFNISCWSRNMKDLICRWTPGAHGETFLHTNYSLKYKLRWYG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cervinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      018985
                                                                                                                                                                                                                     71 LIHECPDYKTGGPNTCYFSKKHTSIWKIYVITVNAINOMGVSSSDPLYVDVTYIVEPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOLUBLE PROLACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       018985;
                                                                                                                                                                                                                                                                      18 NASILNGQS-----PPGKPKIIKCRSPGKETFTCWWEPGSDGG--LPTNYTLTYHKEGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 TYLIQVRCKP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 VYFVQVRCNP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 WPFLRVSW-EPPHKADTRSGWITLIYELRVKLEDEESEWE-NHAAGQQKMFNIFSLRSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 ---LSVRWVSPPALKDF----LFQAKYQIRYRVED-SVDWKVVDDVSNQTSCRLAGLKPGT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
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                                                                                                                                 TSSR 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                           PDVHVSRVGGLEDQLSVRWVS--PPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CFFNKNDTLIWVSYNITVVAINALGKTYSDPVDIDVVYIVKPHPPEKLEVT----VNKDQG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHIPK-DLALFTPYEIWYEATNRLGSARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQ- 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGKPTEITCRSPEKETFTCWWKPGSDGG--LPTTYALYYRKEGSDVVHECPDYHTAGKNS
                                                                                                                                                                                                                                                                                                                               Similarity 33.7 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cervus.
                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                               )41; fn3;
198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TremBirel. 05, Created)
(TremBirel. 05, Last seq
(TremBirel. 08, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                           22652 MW;
                                                                                                                                                                                                                                                                                                                                        15.3%; Score 230.5; 33.7%; Pred. No. 4.6
                                                                                                                                                                                                                                                                                                                                 31;
                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ta; Craniata; Vertebrata; Mammalia;
Ruminantia; Pecora; Cervoidea; Cer
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Last annotation update)
                                                              PRT;
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Pred. No. ]
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ches 76;
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1.2e-15;
                                                                                                                                                                                                                                                                                                                                                   DB 6;
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                                                                                                                                                                                                                                                                                                                                                   Length 198;
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Best Local Similarity
Matches 54; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mustela vison (American mink).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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SEQUENCE
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TORTONESE D.T., BROOKS J., INGLETON P., MCNEIL
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ
EMBL; Y10578; CAA71597.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-WOV-1998 (TrEMBLrel. 08, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM;
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                                                                                                                                                                                                                            114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
                                                                                                                                   173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGEDGG--LPTKYTLTYHKEGETTTHECPDYITSGPNSCYFNKKHTSIWTMYIITINATN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMGSSSSDPRYVTLTYIVEPDPPVNLSL-ELKQPEDKKTYLWIKWYPPTLVDVRSGWLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QYEIRLKPEKATEWE-THFAGLOTQFKILSLYPGQKYLVQVRCKP
                                                                                                                                                                                                                       GETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGS 172
                                                                                                                     ARSDVLTLDVVLDVVTTDPPPDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQI 227
                                          RYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSK 275
                                                                                         SSSDPLYVDVTYIVEPEPPVNLTL-ELKHPEDRKPYLWIKWSPPTLTDVKSGWFSIQYEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00041; fn3;
  RLKPEKATDWE-THFAPKLTQLKIFNLYPGQKYLVQIRCKPDHGYWSE 157
                                                                                                                                                                                                                                                                                              Similarity
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217 AA;
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335 AA;
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                                                                                                                                                                                  -ECPDYKTGGPNSCYFSKKYTSIWKMYVITVSAINQMGI
                                                                                                                                                                                                                                                                           28;
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Pred.
                                                                                                                                                                                                                                                                      Score 203; DB
Pred. No. 4.6e
28; Mismatches
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.4e-13;
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k/DDBJ databases.
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SOOR RAPPOCOS
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Best Local S
Matches 73
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PRESKY D.H., YANG H.,
GATELY M.K., GUBLER U.
Submitted (JUL-1996) t
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99665
                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Entheria: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLIEL 01, 01-NOV-1996 (TrEMBLIEL 01, 01-NOV-1998 (TrEMBLIEL 08, INTERLEUKIN-11 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q16542 PRE
Q16542; Q14626;
                                                                                                                                                  CHEREL M., SOREL M., LEBEAU B., DUBOIS MINVIELLE S., JACQUES Y.;
Molecular cloning of two isoforms of hematopoletic cytokine interleukin-l1.
Blood 86:2534-2540(1995).
                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211
TISSUE-PLACENTA;
                                                                Submitted
                                                                                                                                                                                                                                                          MEDLINE; 95399754.
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                                                                                     VAN LEUVEN F.,
                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95
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                EQUENCE OF 3-390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VACTWERGR--DTHLYTEYTLQLSGPKNLTWQKQCKDIYC-DYLDFGINLTPESPESNFT
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                                                            EN F., STAS I
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97134 MW;
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                       FROM N.A
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                                                                HILLIKER C., MIYAKE Y., GOSSLER the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Last sequence update)
Last annotation updat
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Pred. No. 4.
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                                                                                          GOSSLER A.;
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                                                                               Query Match
Best Local :
                                                                 Matches
                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999)
                                                                                                                                                                                                                                  TISSUE-BRAIN, SKELETAL MUSCLE;
MARDA M., YAGUCHI N., HANYUU C., NAKATA Y., ONODA N., TU
KOJIMA T., HABEGAWA M., KIKUCHI Y., NOMURA H.;
"Mouse homolog of human ciliary neurotrophic factor rece
submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF068615, AAC25711.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U32324; AAB36492.1;
EMBL; U32324; CAA86224.1;
EMBL; U32323; AAB36491.1;
EMBL; U32323; CAA86570.1;
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       45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                             QUENCE FROM N.A.
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                         PGATAE---GLYWTLNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVCHARDGSI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRSVKLCC-----PGVTAGDPVSWFRDGEPKLLQGPDSGLGHELVLAQADSTDEGT---
    PCGTASWDAAVTWRVNGTDLAPD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTSYRKKTYLGADSQRRSPSTGPWPC---PQDPLGAARCVVHGAEFWSQYRINVTEVNPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----YICQTLDGALGGTYTLQLGYPPARPV-VSCQAADYENFSCTWSPSQ--ISGLPTRY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSSLQATCSIHGDTPGATA-EGLYWTLNG--RRLPSELSRLLNTSTLALALANLNGSRQQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRVEDSVDWKVVDDVSNQTSCRLAGLK-----PGTVYFVQVRCNPF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ASTRLLDVSLQSILRPDPPQGLRVESVPGYPRRLRASWTYPASWPCQPHFLL--KFRLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SARSDVLTLDVLDVVTTDPPPDVHVSRVGGLEDQLSVRWVSP---PALKDFLFQAKYQIR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLKYKLRWYGODNTCEEYHTVGPHSCHIPKD------LALFTPYEIWVEATNRLG
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                                                                              Similarity
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                                                                                                                                          40831 MW;
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28.1%;
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                                                           Score 172.5;
Pred. No. 5.2e
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation update)
RECEPTOR ALPHA PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -AGLEEVITDAVAGLPHAVRVSARDF 298
                                                                                                                                                      POTENTIAL.
CILIARY NEUROTROPHIC
ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 175; DB 4;
Pred. No. 3.5e-09;
-LLNGSQLILRSLELGHSGLYA----
                                                                                                                                         9A40FE12 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               372 AA
                                                                                       DB 11;
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                                                                                                                                                                    RECEPTOR
 CFHRDSWH 96
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Best Local Similarity
Matches 73; Conserv
              P70225
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01-MAY-1997
01-NOV-1998
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PFAM; PF00041; fn3; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N GATELY M.K., GUBLER U., SUBMITTED YOU THE TOTAL ALL SUBMITTED YOU AND YOU ALL SUBMITTED YOU ALL SUBM
                                                                                                                                                                                                                                            211 VSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 ENGTVACSWNSGK--VTYLKTNYTLQLS----GPNNLTCQKQCFSDNRQNCNRLDLGINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 MK-DLTCRWTPGAHGETFLHTINYSLKYKLRWYGQDN-TCE-EYHTVGPHSC-----HI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Mus musculus (Mouse).
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01-MAY-1997 (TremBirel. 03, Last sequence update)
01-MOY-1998 (TremBirel. 08, Last annotation update)
INTERLEUKIN 12 RECEPTOR, BETA 2 (IL-12 RECEPTOR BETA2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 VTNLSLGMTLFVCKLNCSNSQKKPPVPVC-----GVEISVGVAPEPPQNISCVQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 LINTST-LALALANLNGSRQQSGDNL-VCHARDGSILAGSCLYVGLPPEKPFNISCWSRN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 PTLLIGSSLOATCSIH-----GDTPGATA------EGLYWTLNGRRL-----PSELSR 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77
                                                                                                                                                                      -----EDEGOVVLNQLRYQPLNSTSWNMVNATNAKGKYDLRDLRPFTEYEFQI 310
                                                                                                                                                                                                                                                                                                               SPDLA-ESRFIVRVTAINDLGNSSSLPHTFTFLDIVIPLPPWDIRINFLNASGSRGTLQW
                                                                                                                                                                                                                                                                                                                                                                          PKDLALFTPYEIWVEATNRLGSARSDVLTLDVLDVYTTDPPPDVHVSRVGGLEDQLSVRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVIPLGSAANISCSLNPKOGCSHYPSSNELILLKFVNDVLVENLHGKKVHDHTGHSSTFQ 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKPDPPENVVARPVPSNPRRLEVTWQTPSTWPDPESFPLKFFLRYRPLILDQWQHV-ELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRWYGQDNTCEEYHTVGPHSCHIPKDLALFT--PYEIWVEATNRLGSARSDVLTLDVLDV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAGS-CLYVGLPPEKPFNISCWSRNM-KDLTCRW-----TPGAHGETFLHTNYSLKYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------VCEKDPAL-KNRCHI-RYMHLFSTIKYKVSISVSNALGH-NTTAITEDEFTI 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRHQVLLHVGLPPREPV-LSCRSNTXPKGFYCSWHLPTPTXIPNTFNVTVLHGSKIM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     874 AA;
   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98196 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Mammalia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 171; DB 11; Pred. No. 2.3e-08; 4; Mismatches 115
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9B90EB47 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHUA A.O., NABAVI N.,
   432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  874
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                     210
                                                                                                                                                                                                                                                                                                                                                                                                                                                           203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149
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7 (TrEMBLrel.
7 (TrEMBLrel.
8 (TrEMBLrel.

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Created)
Last sequence update)
Last annotation updat

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Best Local S
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CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                MAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CD1; TISSUE-TESTIS;
MEDLINE; 97129000.
BILINSKI P., HALL M.A., NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERLEUKIN-11 (IL-11RBETA) (I
100 VSGGMVTLKLGFPPARP-EVSCQAVDYENFSCTWSPGQ--VSGLPTRYLTSYRKKTLPGA 156
                                                                                                                                                                                                                                                             IGNAI
                                                                                                                                                                                                                                                                                                                                                                                             I - SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structural analysis of the gene encoding receptor alpha-chain and a related locus. Biol. Chem. 271:13754-13761(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROBB L., HILTON D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CD-1; TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse genome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL11RA2 OR IL-11RBETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Two differentially expressed
                                               49
                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DBB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUENCE FROM N.A
                          75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pha-chain gene (ILllRa2) with
                                                                                                                                                                                                                                                                                                                                                                                                    OF THE RECEPTOR FOR INTERLEUKIN 11.
SUBCULTULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBCULT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
TISSUE SPECIFICITY: HUDELY EXPRESSED.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CONTAINS ONE IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculus (Mouse)
                                                                                                                                                                                                                                                                                                      MGI:109123;
                    SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD
                                                               PGATA-EGLYWTLNGRRLPSELSRLLN--TSTLA--LALANLNGSRQQSGDNLVCHARDG
                                              PGVSAGTPVSWFRDGD-----
                                                                                        Similarity 25.9
63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320:359-363(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HALL M.A., NEUHAUS H.,
                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECEPTOR ALPHA CHAIN 2 PRECURSOR (IL11RA2) INTERLEUKIN-11 RECEPTOR BETA CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                           BELONGS TO THE CYTOKINE FAMILY OF
                                                                                                                                                                     23
432
367
393
1102
1127
1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
                                                                                                                                              46721
                                                                                                  11.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILLSON T.A.,
                                                                                                                                                                                                                                                                  Glycoprotein; Immunoglobulin fold;
                                                                                                                                                                                                                                                                                                                                               JOINED.
JOINED.
                                                                                                                                               ME:
                                                                                        39;
                                           SRLLQGPDSGLGHRLVLAQVDSPDE---GTYVCQTLDG
                                                                                                  Score 165; DB 11;
Pred. No. 3.4e-08;
                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
POTENTIAL.
                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                           INTERLEUKIN-11 RECEPTOR ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin-11 receptor genes
                                                                                                                                              C4FD7DEC
                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a restricted pattern of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BEGLEY C.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GISSEL C.,
                                                                                                                                            N CAA63872).
N CAA63872).
C CRC32;
                                                                                                            DB 11;
                                                                                         105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                murine interleukin-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEATH J.K.,
                                                                                                          Length
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                          RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression.";
                                                                                       36;
                                                                                                                                                                                                                                                                  Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in
                                                                                     Gaps
                                                                 74
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FINAR RARES OF RESERVED TO THE RESERVED TO THE
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                                                                                                                 EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/C, AND C57BL/6; NEUHAUS H., BETTENHAUSEN B. GUENET J.L., GOSSLER A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q64385 PRELIMINARY;
Q64385;
01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
                                                        PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-BALB/C, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOUGH N.M., BEGLEY C.G., METCALE
"Cloning of a murine II-11 recept
gpl30 for high affinity binding
EMBO J. 13:4765-4775(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 97129000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nouse genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOSSLER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dev. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEDLINE; 95045367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILTON D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL-llraLPHA) (ILllral)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIIRAI OR ILIIRA OR ETL2 OR ET12/IL11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
                                                                                                         CONTAINS ONE IG-LIKE D
I- SIMILARITY: BELONGS TO
JBL: X74953; CAA53908.1;
BBL: U14412; AAA53248.1;
BBL: X94162; CAA63873.1;
BBL: X94163; CAA63873.1;
BBL: X94163; CAA63873.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILINSKI P., HALL M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 EPI 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 SILREDPPQGLRVESVPGYPRRLHASWTYPASWRRQPHFLL - - KFRLQYRPAQHPAWSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 NTCEEYHTVGPHSCHIPKD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
TISSUE SPECIFICITY: WIDELY EXPRESSED.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: PART
                                                                                                                                                                                                                                                                                                                                                                                                                                               SUNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESQRESPSTGPWPC--PQDPLEASRCVVHGAEFWSEYRINVTEVNSLG-ASTCLLDVRLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. 320:359-363(1996).
TION: PART OF THE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FEB-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166:521-542(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HILTON A.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      OF THE RECEPTOR FOR INTERLEUKIN WITH LOW AFFINITY, BUT DOES NOT
  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata;
Sciurognathi; Murida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ៥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                              TO THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEUHAUS
Glycoprotein;
POTENTIAL
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F D., NICOLA N.A., WILLSON
ptor alpha-chain; requireme
and signal transduction.";
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Search completed: September 16, 1999, 20:40:09 Job time: 5560 sec

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein protein search, using sw model

Run on: September 17, 1999, 03:08:15; Search time 64.1 Seconds (without alignments)
129.331 Million cell updates/sec

US-09-037-657-25 1919

Title: Perfect score: TLNGRRLPPELSRVLNASTL.....TRGSCPRADGARREVLPDKL 350

Scoring table: BLOSUM62

Database : A_Geneseq_36:*

Searched: 188963 seqs, 23686106 residues

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Query Score Match Length DB

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between the novel HR and a ligand
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aim 18; Page 102-104; 182pp;
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350 AA;
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                                                                                               t, maintenance or regeneration
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13-FEB-1998; US-074721.

01-MAY-1997; US-045287.

01-MAY-1997; US-550030.

13-FEB-1998; US-023890.

(ZYMO ) ZYMOGENETICS INC.

Adams RL, FOSTET DC, Glibert T.

Lok S, Prespell SR, Whitmore TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a Ecytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the lood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
                          W70844 standard; Protein; W70844;
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WPI; 9
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maintenance factor; thyroid; heart; si
cardiac pathology; heart enlargement;
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Zcytor5; cytokinin-111
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13-FEB-1998; US-074721.
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13-FEB-1998; US-023890.
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                       Allelic varaint of human zcytor5. Zcytor5; cytokinin-like receptor; dumaintenance factor; thyroid; heart;
            cardiac pathology;
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Adams RL, Foster DC, Gilbert T, Jelmberg AC, Lehner J
Lok S, Presnell SR, Whitmore TE;
WPI; 99-034662/03.
New mammallan cytokinin-like receptor Zcytor5 - useful down-regulating Zcytor5 natural ligands or detecting
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Zcytor5; cytokinin-like receptor; down-regulation; growth maintenance factor; thyroid; heart; skeletal muscle; cardiac pathology; heart enlargement; Zcytor5 ligand; vari
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Pred. No. 3e-173;
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        down·regulation; growth factor;
t; skeletal muscle; cardiotrophin-1;
en+: %cvtor5 ligand; allelic varaint
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Best Local Similarity
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                                                                      Human Zcytor5 variant.

Zcytor5; cytokinin-like receptor; down-regulation;
zcytor5; cytokinin-like receptor; down-regulation;
maintenance factor; thyroid; heart; skeletal muscl;
maintenance factor; thyroid; heart; Zcytor5 liga;
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05-NOV-1998.
01-MAY-1998; U08865.
13-FEB-1998; US-074721
                                             Homo sapiens. W09849307-A1.
                                                                                                                                    17-MAR-1999
                                                                                                                                                     W70850
                                                                                                                                                                W70850 standard;
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Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
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n-regulating Zcytor5 natu
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llarity 100.0%;
Conservative (
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natural ligands or det
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Pred. No. 3.4e-173;
; Mismatches 0;
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detecting cardiotrophin-l
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e; cardiotrophin-1;
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01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and integrity dentibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.
                                                                                                                   Human Zcytor5 variant.

Zcytor5; cytokinin-like receptor; down

Zcytor5; cytokinin-rike receptor; down

maintenance factor; thyroid; heart; s)

cardiac pathology; heart enlargement;
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WO9849307-A1.
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Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
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01-MAY-1998; US-074721.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
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Adams RL, Foster DC, Gilbert T, Jelmberg Lok S, Presnell SR, Whitmore TE;
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New mammalian cytokinin-like receptor Zc down-regulating Zcytor5 natural ligands
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Sequence 389 AA;
                                                                                                                                                                                                                                                                                                                           Human Zcytor5 variant.
Zcytor5; cytokinin-like receptor; down-regulation;
Maintenance factor; thyroid; heart; skeletal muscle
cardiac pathology; heart enlargement; Zcytor5 ligat
                                                                                                                                                                                                                                                                                                                                                                                                                W70852;
17-MAR-1999
                                                                                                                                                                                                                                                                                       WO9849307-A1.
                                                                                                                                                                                                                                                                                                           Homo sapiens.
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Claim 1; Page 96-97;
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Pred. No. 3.7e-173;
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Best Local Similarity
Matches 349; Conser
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13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
     Claim 1; Page 89-90; 55pp; Engil
The present sequence represents
is a cytokinin-like receptor. So
down-regulate the effects of a
down-regulate the effects of a
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The present sequence represents a Crytor5 wariant protein. Ecytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.
                                                                                             (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
WPI; 99-034662/03.
New mammalian cytokinin-like
                                                                                                                                                                                                                                                              Human Zcytor5 variant.

Human Zcytor5; cytokinin-like receptor; down-regulation; gro
Zcytor5; cytokinin-like receptor; down-regulation; gro
maintenance factor; thyroid; heart; skeletal muscle; c
rardiac pathology; heart enlargement; Zcytor5 ligand;
                                                                 New mammalian cytokinin-like receptor Zcytor5 down-regulating Zcytor5 natural ligands or det in blood
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13-FEB-1998; US-07471.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
Claim 1; Page 91-92; 55pp; English.

The present sequence represents a Zcytor5 variant protein. Zcytor5 is a Cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and t
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L, Foster DC, Gilbert
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Pred. No. 5.7e
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ent; Zcytor5 ligand;
                                                                                                                                              or detecting
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5.7e-173;
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tecting cardiotrophin-1
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Best Local Similarity
Matches 349; Conser
          Claim 1; Page 94-95; 55pp; English.

The present sequence represents a Zcytor5 variant protein. Zcytor5 is a Cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and anti-idiotypic antibody, could be used to purify Zcytor5 and anti-idiotypic antibody.
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(ZYMO ) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
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01-MAY-1997;
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US-074721.
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US-850030.
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natural ligands or detec
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13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
13-FEB-1998; US-023890.
The present sequence represents a Zcytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
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Adams RL,
Lok S, Pre
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maintenance factor; thyroid; heart; skeletal muscl.
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RL, Foster DC, Gilbert
Presnell SR, Whitmore
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The present sequence represents a Zcytor5 variant protein. Zcytor5 is a cytokini-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to test cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects. Sequence 389 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Zcytor5; cytokinin-like receptor; downaintenance factor; thyroid; heart; sicardiac pathology; heart enlargement;
                                                                                                                                                                                              New mammalian cytokinin-like receptor 2, down-regulating Zcytor5 natural ligands
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                                                                                                                                                                                                                                    (2YMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T,
Lok S, Presnell SR, Whitmore TE;
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01-MAY-1997; US-045287
01-MAY-1997; US-850030
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                                                                                                                                                                    99-100; 55pp; English
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ds or detecting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding U4 haematopoletin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease $25 Claim 9; Pagees 29-30; 38pp; English.

This is the amino acid sequence of the human U4 protein from the chamber of the method of the company of the compa
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deficiency, inneceded cancer, and allergy).
                                     181
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Amino acid sequence of the human U4 protein.
Human; U4 protein; haematopoietin receptor superfamily;
cell proliferation; immune response; antibody; cell dif
autoimmune disease; cancer; allergy.
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209831811-A1.
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                                                                                                                                                                   KPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCH
                                                                    HAYCSNLSFRLYDQWRAWMQKSHKTRNQHRTRGSCPRADGARREYLPDKL 350
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                                                                                                                                                                                                                                                                                                                                                                          11 Similarity 100
328; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               93.8%;
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                                                                                                                                                                                                                                                                                                                                                              Score 1800; DB 1, pred. No. 5.5e-162; Pred. No. 5.5e-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 408;
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                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 327; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence represents a protein designated 2cytor5, which a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart block for the collargement. Zcytor5 could be nead to preventing heart block for the collargement.
                                                                                                                                                                                                                                                                                                                                                                                of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
        241
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                                                                                                                                                                                                                      down-regulating Zcytor5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mammalian cytokinin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
WPI, 99-034662/03.
                                                                     181
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                                                                                                                                                                            61 KPYNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCH 120
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GIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKK
                            WVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPF
                                              WVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPF
                                                                                             IPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPEVHVSRVGGLEDQLSVR
                                                                                                            IPKDLALFTPYEIWYEATNRĹGSARSDYLTLDILDVYTTDPPPDVHYSRVGGLEDQLSVR
                                                                                                                                                          KPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytokinin-like receptor; down-regulation; growth
nce factor; thyroid; heart; skeletal muscle; cardi
pathology; heart enlargement; Zcytor5 ligand.
                                                                                                                                                                                                                                                                                            Conservative
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Pred. No. 1.4e
1; Mismatches
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ligands or det
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                                                                                                                                                                                                                                                                                                       DB 1;
.4e-161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detecting cardiotrophin-1
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                                                                                                                                                                                                                                                                                                                      Length 422;
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Best Local Similarity
Matches 326; Conserv
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13-FEB-1998; US-074771.
01-MAY-1997; US-045287.
01-MAX-1997; US-850030.
13-FEB-1998; US-023890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a Zcytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19: Antibodies and therapeutically to modify Zcytor5 ligand effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
Lok S, Presnell SR, Whitmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Zcytor5 variant.

Human Zcytor5; cytokinin-like receptor; down-regulation; granintenance factor; thyroid; heart; skeletal muscle; cardiac pathology; heart enlargement; Zcytor5 ligand.
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W70839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
                                                                                                                                                                                                        121
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283 GIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQPLGWLKK
                    241 GIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRREIKQFIGWIKK 300
                                                                            163
                                                                                                                                                                                                                                              103
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- Search completed: September 17, 1999, 03:08:16 Job time: 307 sec

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Title: September 16, 1999, 20:41:09; Search time 53:94 Seconds (without alignments) 64.033 Million cell updates/sec US-09-037-657-25 1919

Run on:

Perfect score: Sequence:

1 TLNGRRLPPELSRVLNASTL.....TRGSCPRADGARREVLPDKL 350

Searched: Scoring table: BLOSUM62

106577 seqs, 9868381 residues

Database :

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187 LKDFLFQAKYQIRYRVEDSVDWKVV---DDVSNQTSCRLAGLKFGTVYFVQVRCNPFGIY 243

IKSVII-LKYNIQYRTKDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIRC-----M 302

249

244 GSKKAGIWSEWSHPTAASTPRSERP 268

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Query Match 15.1%; Score 290.5; DB 1; Best Local Similarity 28.7%; Pred. No. 4.6e-21; Matches 76; Conservative 46; Mismatches 128;	RESULT 1 US-07-997-556-2 US-07-997-556-2 Sequence 2, Application US/07797556 Patent No. 5262522 GENERAL INFORMATION: Receptor for Oncostatin M and TITLE OF INVENTION: Inhibitory Factor TITLE OF INVENTION: Inhibitory Factor CORRESSOED INTERES: INT	40 160 8.3 908 2 US-08-588-526-3 41 159.5 8.3 383 1 US-08-609-572-2 42 156 8.1 960 2 US-08-588-190-3 43 154.5 8.1 508 2 US-08-850-293-5 44 148 7.7 229 2 US-08-684-687-2 45 145.5 7.6 897 1 US-07-960-389-2 ALIGNMENTS
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303 KEDGKGYWSDWSEEASGIT-YEDRP 326

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
303 KEDGKGYWSDWSEEASGIT-YEDRP 326
                                 244 GSKKAGIWSEWSHPTAASTPRSERP 268
                                                                                           187 LKDFLFQAKYQIRYRVEDSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIY 243
                                                                                                                                   190 YFVNIEVWVEAENALGKVTSDHINFDPVYKVKPNPPHNLSVINSEELSSILKLTWTN-PS
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                                                                                                                                                                     LFTPYEIWYEATNRLGSARSDYLTLDILDVYTTDPPPDVHVSRVGGLEDQLSVRWVSPPA 186
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                                                                                                   187 LKDFLFQAKYQIRYRVEDSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIY 243
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                                                                                                                                       190 YFVNIEVWYEAENALGKYTSDHINFDPYYKYKPNPPHNLSVINSEELSSILKLTWTN-PS 248
                                                                                                                                                                         127 LFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPA 186
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303 KEDGKGYWSDWSEEASGIT-YEDRP 326
                                 244 GSKKAGIWSEWSHPTAASTPRSERP 268
                                                                   249 IKSVII-LKYNIQYRTKDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIRC---
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16; Mismatches 128;
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                                                                                                                                                                                                                                               108 CEEYHTVGPHSCHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPP---- 163
                                                                                                                                                                            163 ----PDVHVSRVGGLEDQLSVRWVS-PPALKDFLFQAKYQIRYRVE-DSVDWKVVDDV-S 215
                                                                                                                                                                                                                176 PDCVAKKRONNCSIPRKNLLLYQYMAIWVQAENMLGSSESPKLCLDPMDYVKLEPPMLQA 235
                                                                                                                                                                                                                                                                                        118
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OPERATING SYSTEM:
                                                                    289 SKDQFELCGLHQAPVYTLQMRC----IRSSLPGFWSPWSPGLQLRPTMKAPTIRLDT-- 342
                                                                                                                                           236 LDIGPDVVSHQPGCL-----WLSWKPWKPSEYMEQECELRYQPQLKGANWTLVFHLPS
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342 ----WCQKKQLDPGTVSVQLFWKPTPLQEDSGQIQGYL-
                                   270 PGGGACEPRGGEPSS------GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQ 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                           FILING DATE: 22-MAR-1991
TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                        NQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWS-----HPT-AASTPRSERPG 269
                                                                                                                                                                                                                                                                                        LHAGYPPASPSNLSCLMHLTINSLVCQWEPGP--ETHLPTSFILKSFRSRADCQYQGDTI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: Jones, Tullar & F: P.O. Box 2266 Eads Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                Score 241;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 837;
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Best Local Similarity
70; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIOR APPLICATION DATA:
                                                                108 CEEYHTVGPHSCHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDILDVV-----T 158
159 TDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVE-DSVDWKVVDDVSNQ 217
                                     175
                                                                                                117 LRAGYPPAIPHNLSCLMNLTTSSLICQWEPGP--ETHLPTSFTLKSFKSRGNCQTQGDSI 174
                                                                                                                                53 LYVGLPPEKPVNISC-WSKNMKDLTCRWTPGAHGETFLHTNYSLK-YKLRWYGQ---DNT 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                           ECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   EFERENCE/DOCKET NUMBER:
                                   LDCVPKDGQSHCCIPRKHLLLYQNMGIWVQAENALGTSMSPQLCLDPMDVVKLEPPMLRT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION
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                                                                                                                                                                                                                                                                TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ION NUMBER:
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P.O. Box 2266 Eads Station
                                                                                                                                                                  Conservative
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SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER:
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                                                                                                                                                                                    Score 220.5;
Pred. No. 6.7
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                                                                                                                                                                                 6.7e-14;
                                                                                                                                                                                                     DB 1;
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218 T-SCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWS 255

MDPSPEAAPPQAGCIQ----LCW--EPWQPGLHINQKCELRHKPQRGEASWALVGPLPLE 288

Gaps

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289 ALQYELCGLLPATAYTLQIRCIRWPL----PGHWSDWS 322

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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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289 ALQYELCGLLPATAYTLQIRCIRWPL-
                           218 T-SCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWS 255
                                                                                159 TDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVE-DSVDWKVVDDVSNQ
                                                                                                             175 LDCVPKDGQSHCCIPRKHLLLYQNMGIWVQAENALGTSMSPQLCLDPMDVVKLEPPNLRT 234
                                                     235 MDPSPEAAPPQAGCLQ----LCW--EPWQPGLHINQKCELRHKPQRGEASWALVGPLPLE
                                                                                                                                        108 CEEYHTVGPHSCHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDILDVV-----T 158
                                                                                                                                                                   117 LRAGYPPAIPHNLSCLMNLTTSSLICQWEPGP--ETHLPTSFTLKSFKSRGNCQTQGDSI 174
                                                                                                                                                                                                53 LYYGLPPEKPYNISC-WSKNMKDLTCRWTPGAHGETFLHTNYSLK-YKLRWYGQ---DNT 107
                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                      l Similarity 32.(70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P: P.O. Box 2266 Eads Station Arilington
                                                                                                                                                                                                                                                                                                                              TYPE:
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                                                                                                                                                                                                                                                                                                                                                                      71 amino acids
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22-MAR-1991
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                                                                                                                                                                                                                                                    11.5%;
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Colony-Stimulating Factor Receptor
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                                                                                                                                                                                                                                                 Score 220.5; DB Pred. No. 6e-14;
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                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                   , 68
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                                                                                                            175 LDCVPKDGQSHCCIPRKHLLLYQNMGIWVQAENALGTSMSPQLCLDPMDVVKLEPPMLRT
                                                                                                                                         108 CEEYHTVGPHSCHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDILDVV------T 158
                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
289 ALQYELCGLLPATAYTLQIRCIRWPL--
                          218 T-SCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWS 255
                                                    235 MDPSPEAAPPQAGCLQ----LCW--EPWQPGLHINQKCELRHKPQRGEASWALVGPLPLE
                                                                                159 TDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVE-DSVDWKVVDDVSNQ
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                                                                                                                                                                                                   53 LYVGLPPEKPVNISC-WSKNMKDLTCRWTPGAHGETFLHTNYSLK-YKLRWYGQ----DNT 107
                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT
FILING DATE: 22-MAR-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 03-JU
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                                                                                                                                                                     LRAGYPPAIPHNLSCLMNLTTSSLICQWEPGP--ETHLPTSFTLKSFKSRGNCQTQGDSI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TER READABLE FORM:
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                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                      11.5%;
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PGHWSDWS 322
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                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                  Length 863;
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NFORMATION FOR SEQ
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                                                                                                                                                                                                                                159 AL-KNRCHI-RYMHLESTIKYKVSISVSNALGH-NATAITEDEFTIVKPDPPENVVARPV 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                   171
                                                                                                                                                                                                                                                                     113 TYGPHSCHIPKDLALFT -- PYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRV 170
328 PPPTTKICDPGELGSGGGPCAP 349
                                         269 ---
                                                                     275 EYIIQYAAK-----DNEIGTWSDWS-VAAHATPWTEEPRHLTTEAQAAETTTSTTSSLA 327
                                                                                                                 230 VYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERP--
                                                                                                                                                  216 PSNPRRLEVTWQTPSTWPDPESFPLKFFLRYRPLILDQWQHV-ELSDGTAHTITDAYAGK 274
                                                                                                                                                                                                                                                                                                                  111 EPV-LSCRSNTYPKGFYCSWHLPTPTYIPNTFNVTVLHGSKIM----
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                                                                                                                                                                                                                                                                                                                                                                                        59 VNGTDLAPDL---LNGSQLV-----LHGLELGHSGLYACFHRDSWHLRHQVLLHVGLPPR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             2 LNGRRLPPELSRYLNASTLALALANLNGSRQRSGDNLYCHARDGSILAGS-CLYYGLPPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERATING SYSTEM:
                                                                                                                                                                                       GGLEDQLSVRWVSPPALKD-FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGT 229
                                                                                                                                                                                                                                                                                                                                                   KPVNISCWSKNM-KDLTCRW------TPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATION NUMBER: US/07/801/562
DATE: 02-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Yor
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1155 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 8698864/9741
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                                     -GPGGGACEP 277
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N: Cell Free Ciliary Neurotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.4%;
26.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 219.5; DB 1;
Pred. No. 2.7e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
328 PPPTTKICDPGELGSGGGPCAP 349
                                                                          275 EYIIQYAAK-----DNEIGTWSDWS-VAAHATPWTEEPRHLTTEAQAAETTTSTTSSLA 327
                                                                                                                                                                                                                                         159 AL-KNRCHI-RYMHLFSTIKYKVSISVSNALGH-NATAITFDEFTIVKPDPPENVVARPV 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                      230 VYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERP--
                                                                                                                                                          216 PSNPRRLEVTWQTPSTWPDPESFPLKFFLRYRPLILDQWQHV-ELSDGTAHTITDAYAGK 274
                                                                                                                                                                                                                                                                                                                              111 EPV-LSCRSNTYPKGFYCSWHLPTPTYIPNTFNVTVLHGSKIM--
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                                                                                                                                                                                                                                                                                                                                                                                                      59 VNGTDLAPDL---LNGSQLV-----LHGLELGHSGLYACFHRDSWHLRHQVLLHVGLPPR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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FILING DATE: 19910328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGS-CLYVGLPPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                                                                                                                                                                 GGLEDQLSVRWYSPPALKD-FLFQAKYQIRYRYEDSVDWKVVDDVSNQTSCRLAGLKPGT 229
                                                                                                                                                                                                                                                                                 TVGPHSCHIPKDLALFT -- PYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRV 170
                                                                                                                                                                                                                                                                                                                                                                KPVNISCWSKNM-KDLTCRW------TPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGENT INFORMATION: Misrock, S. Leslie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66141
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1155 Avenue of the
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ENTION: The Ciliary Neurotrophic Factor Receptor
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                                        GPGGGACEP 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.4%; Score 219.5; DE 26.7%; Pred. No. 2.7e-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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328 PPPTTKICDPGELGSGGGPCAP 349

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                                     275 EYIIQVAAK---
                                                                                                        216 PSNPRRLEVTWQTPSTWPDPESFPLKFFLRYRPLILDQWQHV-ELSDGTAHTITDAYAGK
                                                                                                                                         171 GGLEDQLSVRWYSPPALKD-FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGT
                                                                                                                                                                                                                    113 TVGPHSCHIPKDLALFT--PYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                    230 VYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERP-----
                                                                                                                                                                                                                                                         111 EPV-LSCRSNTYPKGFYCSWHLPTPTYIPNTFNVTVLHGSKIM-------VCEKDP 158
                                                                                                                                                                                                                                                                                              61 KPYNISCWSKNM-KDLTCRW-----TPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYH 112
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                    59 VNGTDLAPDL---LNGSQLV-----LHGLELGHSGLYACFHRDSWHLRHQVLLHVGLPPR 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                       2 LNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGS-CLYVGLPPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                  AL-KNRCHI-RYMHLESTIKYKVSISVSNALGH-NATAITFDEFTIVKPDPPENVVARPV
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APPLICATION DATA:
US_07/700,677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                               ---DNEIGTWSDWS-VAAHATPWTEEPRHLTTEAQAAETTTSTTSSLA 327
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GPGGGACEP 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                    11.4%; Score 219.5; 26.7%; Pred. No. 2.
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275 EYIIQVAAK------DNEIGTWSDWS-VAAHATPWTEEPRHLTTEAQAAETTTSTTSSLA 327
                                                                                                                  171 GGLEDQLSVRWVSPPALKD-FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGT
                                                                           216 PSNPRRLEVTWQTPSTWPDPESFPLKFFLRYRPLILDQWQHV~ELSDGTAHTITDAYAGK 274
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                                                                                                                                                       159 AL-KNRCHI-RYMHLESTIKYKVSISVSNALGH-NATAITFDEFTIVKPDPPENVVARPV 215
                                                                                                                                                                                          113 TYGPHSCHIPKDLALFT--PYEIWVEATNRLGSARSDYLTLDILDVYTTDPPPDVHVSRV 170
                                                                                                                                                                                                                                       111 EPV-LSCRSNTYPKGFYCSWHLPTPTYIPNTFNVTVLHGSKIM--
                                           230 VYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERP-----
                                                                                                                                                                                                                                                                        61 KPVNISCWSKNM-KDLTCRW-----TPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYH 112
                                                                                                                                                                                                                                                                                                                 59 YNGTDLAPDL---LNGSQLV-----LHGLELGHSGLYACFHRDSWHLRHQVLLHVGLPPR 110
                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                    2 INGRRIPPEISRVINASTIALALANINGSRQRSGDNLVCHARDGSILAGS-CLYVGLPPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELEPHONE: 212 790-9090
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                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 8698864/9741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ancopoutos,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                               11.4%; Score 219.5; DB 2; Length 372; 26.7%; Pred. No. 2.7e-14; ative 37; Mismatches 122; Indels 77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stephen P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 07/676,647
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of the Americas
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                171 GGLEDQLSVRWVSPPALKD-FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
          275 EYIIQVAAK---
                                   230 VYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERP--
                                                               216 PSNPRRLEVTWQTPSTWPDPESFPLKFFLRYRPLILDQWQHV-ELSDGTAHTITDAYAGK 274
                                                                                                                                159 AL-KNRCHI-RYMHLFSTIKYKVSISVSNALGH-NATAITFDEFTIVKPDPPENVVARPV 215
                                                                                                                                                                 113 TYGPHSCHIPKDLALET---PYEIWYEATNRLGSARSDYLTLDILDVYTTDPPPDVHYSRY 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                   61 KPVNISCWSKNM-KDLTCRW-----TPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYH 112
                                                                                                                                                                                                                                                                    59 VNGTDLAFDL---LNGSQLV-----LHGLELGHSGLYACFHRDSWHLRHQVLLHVGLPPR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 PPPTTKICDPGELGSGGGPCAP 349
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                                                                                                                                                                                                        EPV-LSCRSNTYPKGFYCSWHLPTPTYIPNTFNVTVLHGSKIM--
                                                                                                                                                                                                                                                                                                    LNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGS-CLYVGLPPE 60
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                                                                                                                                                                                                                                                                                                                                                 86;
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                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Squinto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davis, Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Annopoulos, George D.
SNTION: The Ciliary Neurotrophic Factor Receptor
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-DNEIGTWSDWS-VAAHATPWTEEPRHLTTEAQAAETTTSTTSSLA 327
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                                                                                                                                                                                                                                                                                                                                                          11.4%; Score 219.5;
26.7%; Pred. No. 2.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                       2.7e-14;
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                                                                                                                                                                                                                                                                                                                                                                          Length 372;
                                                                                                                                                                                                     --VCEKDP 158
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Best Local Similarity
                                                                                                                                                                                          Matches
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                            164 DVHVSRVGGLEDQLSVRWYSPPALKDFLFQAKYQIRYRVE-DSVDWKVVVDDVSNQT-SCR 221
121 EAAPPQAGCLQ----LCW--EPWQPGLHINQKCELRHKPQRGEASWALVGPLPLEALQYE 174
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 602 amino acids
                                                                                        113 TYGPHSCHIP-KDLALFTPYEIWVEATNRLGSARSDYLTLDILDVV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy
                                                          61 KDGQSHCCIPRKHLLLYQNMGIWVQAENALGTSMSPQLCLDPMDVVKLEPPMLRTMDPSP
                                                                                                                                                 58 PPEKPVNISC-WSKNMKDLTCRWTPGAHGETFLHTNYSLK-YKLRWYGQ---DNTCEEYH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269
                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 PPPTTKICDPGELGSGGGPCAP 349
                                                                                                                     3 PPAIPHNISCLMNLTTSSLICQWEPGP--ETHLPTSFTLKSFKSRGNCQTQGDSILDCVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/248,532 FILING DATE: 31-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                             OPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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: United States of America
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                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                               Region
1..602
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                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ON DATA:
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                                                                                                                                                                                                                                                                                                                                                                        protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235-3500
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                                                                                                                                                                                                  11.1%; Score 213.5; DB 2
31.8%; Pred. No. 2.1e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERLEUKIN-12 RECEPTOR
                                                                                                                                                                                                                                                                              factor-receptor
                                                                                                                                                                                                                                                                                      /note= "Represents residues 98 to 731 of human granulocyte colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 08/094,713
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                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                  Indels
                                                                                                                                                                                                                Length 602;
                                                                                        ---TTDPPP 163
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                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                         209 SSSLPSTFTFLDIVRPLPPWDIRIKFQKASVSRCTLYW-----RDEGLVLLNRLRYRPS 262
318 EEEPTG 323
                                                                                                       204 DSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 263
                                                                                                                                                                                144 ARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVE 203
                                                                                                                                                                                                                161 LSGPKNLTWOKOCKDIYC-DYLDFGINLTPESPESNFTAK-----VTAVNSLGS 208
                                  264 RSERPG 269
                                                                                                                                                                                                                                                   97 Y----KLRWYGQ--DNTCEEYHTVG-----PHSCHIPKDLALFTPYEIWVEATNRLGS 143
                                                                                                                                                                                                                                                                                         103 LACINSDEIQICGAEIFVGVAPEQPQNLSCIQKGEQGTVACTWERGR--DTHLYTEYTLQ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 LCGLLPATAYTLQIRCIRWPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWS 255
                                                                                                                                                                                                                                                                                                                            38 LVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMK-DLTCRWTPGAHGETFLHTNYSLK 96
                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                        NSRLWNMVNVTKAKGRHDI
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IUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERENCE/DOCKET NUMBER:
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MT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   862 amino acids
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Presky, David H
PRESKY, DECEPTORS FOR HUMAN IL-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                     10.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD 9195
                                                                                                                                                                                                                                                                                                                                                                                     Score 207.5;
Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                    104;
                                                                                                                                                                                                                                                                                                                                                                    Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 862;
                                                                    KGSWSDWSESLRAQTP 317
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Best Local :
                                                                                                                                                                                                                                                                                                                                                               Matches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARAC
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APPLICATION NUMBER:
                                                                                                                                                                                                                     161
318 EEEPTG 323
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                                                                                                                                            209 SSSLPSTFTFLDIVRPLPPWDIRIKFQKASVSRCTLYW---
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RESULT 15

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prolactin receptor - human (fragment) C;Species: Homo sapiens (man) C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996 C;Accession: A57018 R;Fuh, G; Wells, J.A. J. Biol. Chem. 270, 13133-13137, 1995 A;Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell A;Reference number: A57018; MUID:95286597 A;Accession: A57018 A;Scatus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Molecule type: mRNA	73 165 133 133 191	references: GDB:12031: spition: 5pi3.3-5pi3.1 cds: glycoprotein; tran cds: glycoprotein; tran comain: signal sequence //Product: prolactin re //Product: prolactin re //233/Binding site: can Match 17.3 ocal Similarity 37.1 ss 83; Conservative ss; 5 LFLNTCLLNGQLPPGKPEIF	ISULT 1 10144 10144 1014 1014 1014 1014 1014 Include Homo sapiens (man) Date: 17-U1-1992 #sequence_revisi Accession: A40144 Boutin, J.M.; Edery, M.; Shirota, I 1. Endocrinol. 3, 1455-1461, 1989 Title: Identification of a cDNA en Reference number: A40144; MUID:901: Accession: A40144 MOlecule type: mRNA Residues: 1-622 <boud cross-references:="" gb:m31661;="" genetics:="" genetics:<="" nid:g="" td=""><td>40 170 8.9 1162 2 PC4184 41 170 8.9 805 3 JC4897 leptin receptor, 0 42 169 8.8 265 2 S14081 erythropoietin rec 43 166 8.7 1092 2 JX0312 differentiation-st 44 166 8.7 719 2 JC2181 differentiation-st 45 165.5 8.6 440 2 JL0144 interleukin-6 rece</td></boud>	40 170 8.9 1162 2 PC4184 41 170 8.9 805 3 JC4897 leptin receptor, 0 42 169 8.8 265 2 S14081 erythropoietin rec 43 166 8.7 1092 2 JX0312 differentiation-st 44 166 8.7 719 2 JC2181 differentiation-st 45 165.5 8.6 440 2 JL0144 interleukin-6 rece

A;Molecule type: mRNA A;Residues: 1-206 <RES> A;Cross·references: GB:S78505; NID:g999114; PID:g999115

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Endocrinology 135, 269-276, 1994
A;Title: Cloning, expression, and mutational analysis
A;Reference number: I50455; MUID:94283267
A;Accession: I50455
A;Status: preliminary; translated from GB/EMBL/DDBJ
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ndocrinology 135, 269-276, 1994
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                                                    lochem. Biophys. Res. Commun. 168, 415-422, 19; Title: Isolation and characterization of two Reference number: A34631; MUID:90241201; Accession: A34631
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                                       Status: preliminary
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J. Biol. Chem. 266, 20110-20117, 1991
A; Title: A prolactin-dependent immune cell
A; Reference number: A41070; MUID:92041834
                                                       C; Accession: A41070; I55417
R; Ali, S.; Pellegrini, I.;
                                                                                               prolactin receptor Nb2 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shirota, M.; Banville, D.; Ali, S.; ol. Endocrinol. 4, 1136-1143, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: A36116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Date: 28-Mar-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 79; Conserv
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the authors translated
                                                                                                                                                                                                                                                                                                                            RNLTL-EVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ
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                                                           I.; Kelly, P.A.
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35.0%;
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the codon GAG for residue 533 as Gly
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Pred. No. 8.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 313; DB 2;
Pred. No. 8.4e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Residues: 1-310 <B0U>
;Cross-references: GB:M19304; NID:g206364; PID:g206365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Molecule type: mRNA
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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20-310/Product: prolactin receptor #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title: Cloning and expression of the rat prolactin receptor, Reference number: A29884; MUID:88165059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Rattus norvegicus (Norway rat)
Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 20-Mar-1998
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              Keywords: transmembrane protein
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. Biol. Chem. 269, 26076-26082, 1994
.Fille: Differential signal transduction of the short, Nb2, and long prolactin receptor;Reference number: I55417; MUID:95014432
.Accession: I55417
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126 RNLTL-EVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ
                                         163 PDVHVSRVGGLEDQLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ 217
                                                                                                                         106 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPP 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, M.; 69-77, 1988
                                                                                                                                                                         SLLKGQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                                                                    TTYECPDYKTSGPNSCFFSKQYTSIWKIYITTVNATNQMGSSSSDPLYVDVTYIVEPEPP 125
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Pred. No. 3.5e-20;
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Pred. No. 5.1e-20;
96; Mismatches 85;
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A; Residues: 1-292 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-1996
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                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-303 <RE
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                                                                                                                                                                           Query Match
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Date: 02-Aug-1996 #sequence_revision 02-Aug-1996
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1. Endocrinol. 3, 674-680, 1989
                                                                                                                                                                                                                                                                                                                                                                                     Endocrinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 TITDYKTGWFTMEYEIRLKSEEADEWE-IHFTGHQTQFKVFDLYPGQKYLVQTRCKP---
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                                                                             11 LSRVLNASTLALALANINGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 YGSKKAGIWSEWSHPTAASTP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 ALKDF --- LFQAKYQIRYRVEDSYDWKYVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 242
                                                                                                                                                        Local Similarity
71 NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNT--CEEYHTVGPHSCHIPKD-LAL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 TQFKVFDLYPGQKYLVQTRCKP-----DHGYWSRWSQESSVEMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNT--CEEYHTVGPHSCHIPKD-LAL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSRVLNASTLALALANINGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKETFTCWWNPGSDGG--LPTNYSLIYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSSALAYMLLVLSISLLNGQS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-303 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DHGYWSRWGQEKSIEIP 222
                                                                                                                                                                                                                                                                                                                                                                             inzer, D.I.H.
3, 674-680, 1989
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                  16.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.1%; Score 309.5; DB 2
31.4%; Pred. No. 6.9e-20;
tive 38; Mismatches 94
                                                                                                                              38;
                                                                                                                      Score 309.5; DB 4;
Pred. No. 6.6e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------PPGKPEIHKCRSP 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #text_change 02-Aug-1996
                                                                                                                                                                 Length 292;
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 303;
                                          PPGKPEIHKCRSP 34
                                                                                                                          47;
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                                                                                                                                                                                                                                                                                                                                                       mouse liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1-557,'F',559-608 <EDE>
(Cross-references: EMBL:X73372; NID:g312696; PID:g312697)
(Comment: Prolactin receptor have long form and short form whiteComment: This long form receptor is capable of transducing a Reywords: receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.;Reference number: S34356;Accession: S34356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form Reference number: JT0671; MUID:94085788 Accession: JT0671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clarke, D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Mus musculus (house mouse)
Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 29-Jan-1999
Accession: I53299; JT0671; S34356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
Residues: 1-608 <MOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:L14811; NID:g293769; PID:g293770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title: Changes in prolactin receptor expression during Reference number: I53269; MUID:93307149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       docrinology 133,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: mRNA
Residues: 1-608 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tatus: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lactin receptor, long form -
                                                       186
                                                                                                                                      128
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mes 82; Conserv
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                                                                                                                                                                                                                                                                1 MSSALAYMLLVLSISLLNGQS---
                                                                                    WKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP
                                                                                                                         FTPYEIWVEATHRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVS--pP
                                                                                                                                                                                                                                                                                                 LSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSK 70
                                            ALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 242
                                                                                                                                                                     DKETFTCWWNPGSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI 90
    TITDVKTGWFTMEYEIRLKSEEADEWE-IHFTGHQTQFKVFDLYPGQKYLVQTRCKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITDVKTGWFTMEYEIRLKSEEADEWE-IHFTGHQTQFKVFDLYPGQKYLVQTRCKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKETFTCWWNPGSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI
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                                                                                                                                                                                                                                                                                                                                                                      16.1%;
                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                Score 309.5; DB 2;
Pred. No. 1.7e-19;
98; Mismatches 94;
                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                                       608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signal
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C;Species: Gallus gallus (chicken
C;Date: 30-Sep-1993 #sequence_rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number:
A;Accession: JQ1655
                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Keywords: glycoprotein; transmembrane protein
;1-23/Domain: signal sequence #status predicted <SIG>
;24-831/Product: prolactin receptor #status predicted <MAT>
;439-462/Domain: transmembrane #status predicted <TMM>
;59.91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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10chem. Biophys. Res. Commun. 188, 490-496, 1992
Fittle: Double antenna structure of chicken prolactin
Reference number: JQ1655; MUID:93075121
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: DDBJ:D13154; NID:g222848; PID:d1002939;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: JQ1655
                                                                                                                                                                                                         117 HSCHI-PKDLALFTPYEIWVEATNRLGSARSDYLTLDILDVVTTDPPPDV--HVSRVGGL 173
      405
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                                                231
                                                                                                                      174 EDQLSVRWVSPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV 230
                                                                                                                                                                                                                                                   230 PPEKPTIIKCRSPEKETFTCWWKPGLDGG---HPTNYTLLYSKEGEEQVYECPDYRTAGP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
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                                                                                                                                                                                                                                                                                        58 PPEKPVNISCWSKNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
YIIQIHCKP-----DHHGSWSEWSSENYIQIPNDFR 435
                                         YFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSER 267
                                                                                 KPYLVLTW-SPPPLADVRSGWLTLEYELRLKPEEGEEWETI-FVGQQTQYKMFSLNPGKK 404
                                                                                                                                                                NSCYFDKKHTSFWTIYNITVRATNEMGSNSSDPHYVDVTYIVQPDPPVNVTLELKKPINR 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- DHGYWSRWGQEKSIEIP 222
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75; Conserv
                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                            Score 308; DB 2;
Pred. No. 3.4e-19;
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C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Feb-1997
C;Accession: I45971
R;Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A;Title: Molecular cloning of the bovine prolactin receptor and distribution A;Reference number: I45971; MUID:93246019
A;Accession: I45971 A; Gene: A; Status: preliminary; translated from GB/EMBL/DDB: A;Cross-references: GB:L02549; NID:g163617; PID:g163618 A; Molecule type: mRNA A; Residues: 1-581 <SCO> prolactin receptor - bovine Query Match Best Local S Matches 81 Similarity Conservative 16.0%; Pred. No. 2. Mismatches .9e-19; ຸນ Indels Length 47; distribution of prol Gaps 9

12 SRVLNASTLALANLNGSRORSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKN 71

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glycoprotein
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Residues: 41-58, 'X', 60-66;90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX', 167
Residues: 41-58, 'X', 60-66;90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX', 167
Residues: 41-58, 'X', 60-66;90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX', 167
Residues: 41-58, 'X', 60-66;90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX', 167
Residues: 41-58, 'X', 60-66;90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX', 167
Residues: 41-58, 'X', 60-66;90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX', 167
Residues: 41-58, 'X', 60-66;90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX', 167
Residues: 41-58, 'X', 60-66;90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX', 167
Residues: 41-58, 'X', 60-66;90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX', 167
Residues: 41-58, 'X', 60-66;90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX', 167
Residues: 41-58, 'X', 60-66;90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX', 167
Residues: 41-58, 'X', 96-66, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX', 167
Residues: 41-58, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX', 167
Residues: 41-58, 'X', 96-66, 'X', 98-103, 'X', 105, 'X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:J04510; NID:g165669; PID:g165670
Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.;
L. J. Blochem. 22, 1089-1095, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Orycto
Date: 07-Sep-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: Purification and partial sequence of the rabbit mammary gland Reference number: A60380; MUID:91146782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: mRNA
Residues: 1-616 <EDE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: A30304
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lternate names: prolactin receptor, mammary gland
                                                                                                                                                                                                                                                                                                                                                       177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
                                                                                                                                                              203
                                                                                                                                                                                                                      232 FVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 263
                                                                                                                                                                                                                                                                                     144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 --- DHGYWSEWSPESSIQIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 GSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 YEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWV--SPPALK 188
                                                                                                                                                                                                                                                                                                                                                                                                                   85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 PPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTGEEYHTVGPH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                  KPYLWVKWLPPTLVDVRSGWLTLQYEIRLKPEKAAEWE-THFAGQQTQFKILSLYPGQKY 202
                                                                                                                                                                                                                                                                                                                                             LSVRWVS--PPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQ
                                                                                                                                                                                                                                                                                                                                                                                                            SCYFSKKHTSIWTIYIITVNATNQMGSSVSDPRYVDVTYIVEPDPPVNLTL-EVKHPEDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPGKPFIFKCRSPEKETFTCWWRPGADGG--LPTNYTLTYHKEGETITHECPDYKTGGPN 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-----FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIY 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHI-PKDLALFTP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KETFTCWWEPGADGG--LPTNYTLTYHKEGETLIHECPDYKTGGPNSCYFSKKHTSIWKM 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YVITVNAINQMGISSSDPLYVHVTYIVEPEPPANLTL-ELKHPEDRKPYLWIKWSPPTMT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRVVFILLLFLSVSLLNGQS-
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130
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mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 300.5; DB 2
; Pred. No. 1.1e-18;
29; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (domestic rabbit) vision 07-Sep-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Henzel, W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.; Dusanter-Fourt, I.; Petridou,
6, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #text_change 20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPEKPKLVKCRSPG
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                                                                                                                                                                                                                                                                                                                                                                                                         143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B.; Boutin
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                                                                                                                                                                                                                               Cell 63, 1149-1157, 1990
A;Title: Molecular cloning and expression of
A;Reference number: A36337; MUID:91084844
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                   A; Cross-references: GDB:
A; Map position: 5q11-5q1
                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                  membrane glycoprotein gp130 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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A;Title: Molecular cloning of a murine IL-6
A;Reference number: 148370; MUID:92291532
A;Accession: 149699
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Mus musculus (house mouse; C; Date: 02-Aug-1996 #sequence_revision)
                                                                    A; Gene: GDB: IL6ST; GP130
                                                                                                                                                                                                         A; Accession: A36337
                                                                                                                                                                                                                                                                                                                                C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X62646; NID:g840816; PID:g840817
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A;Residues: 1-917 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Saito,
                                                                                                                                          ;Molecule type: mRNA
;Residues: 1-918 <HIB>
                                                                                                                  Cross-references:
                                                                                                                                                                                      Status: preliminary
                                                                                                                                                                                                                                                                                                     Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: I48370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 PFGIYGSKKAGIWSEWSHPTAAST--PRSERP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 VSPPALKDFLFQAKYQIRYRVEDSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 SYMPTYYVNIEVWVEAENALGKVSSESINFDPVDKVKPTPPYNLSVINSEELSSILKLSW 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 PKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRW 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 VNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGOD-NTCEEYHTVGPHSCHI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 NGRRLPPELSRYLNASTLALALANLNGSRQRSGDNLYCHARDGSILAGSCLYYGLPPEKP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --SIKDSGK-GYWSDWSEEASGTTYEDRPSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSSGL--GGLLDLKSDIQYRTKDASTWIQVPLEDTMSPRTSFTVQDLKPFTEYVTRIR-- 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNLTCIVNEGKNMLCQWDPGR--ETYLETNYTLKSE--WATEKFPDCQSKHGT---SCMV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NHAAVPREQVTVINRTTSSVTFTDVVLPSVQLTCNILSFGQIEQNVYGVTMLSGFPPDKP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translated from
glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                               GB:M57230; NID:g186353; PID:g186354
                                           GDB:126725; OMIM:600694
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membrane protein
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Pred. No. 3.6e-18;
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. Similarity 76; Conserv

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187 LKDFLFOAKYQITYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIY 243 :
OF CWSKNINGLICKMTPGARGETFLITNYSLKYKLRWYGGONTCEETHTVGPHSCHIPKDLA 126

Search completed: September 16, 1999, 20:42:10 Job time: 5403 sec

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GenCore version Copyright (c) 1993 - 1998
Compugen Ltd.
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Run on: OM protein protein search, using sw model

September 17, 1999, 03:10:14; Search time 35.09 Seconds (without alignments) 281.958 Million cell updates/sec

ritle: equence: erfect score: US-09-037-657-25 1919

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earched: coring table: BLOSUM62

vatabase : SwissProt_37:* 77977 seqs, 28268293 residues

Pred. No. No. is the number of results predicted by chance to have greater than or equal to the score of the result being pr s derived by analysis of the total score distribution. printed

SUMMARIES

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or send an email to license@isb-sib.ch
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"The X-ray structure of a growth hormone-prolactin receptor complex.";
NATURE 372:478-481(1994).
                                                                                                                 use by non-profit institute nodified and this statement
                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                         his SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALI S., GOULD D., DJIANE J., KELLY P.A.; "Identification of a cDNA encoding a long form of prolactin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235
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I; HOMINIDAE; HOMO.
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CARBOHYD CARBOHYD CARBOHYD DISULFID SEQUENCE MAIN OMAIN EMBL; м31661; G190362; -ROSITE; PS00241; RECEPTOR_CYTOKINES_1; 1. ROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1. 23-SEP-98. A40144 RANE; GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE 69505 MW; POTENTIAL.
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6924E155 CRC32; BY SIMILARITY.
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EXTRACELLULAR (POTENTIAL). POTENTIAL

Query Match
Best Local Similarity
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Score 332; DB 1; 1 Pred. No. 4.7e-21; B; Mismatches 95;

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01-NOV-1997 (REL. 39
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PROLACTIN RECEPTOR 1
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                                                                                                                               DOMAIN
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                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foundaties requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLUMBA LIVIA (DOMESTIC PIGEON).
EUKARYOTA; METAZOA; CHORDATA; VE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHEN X., HORSEMAN N.D.;
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EXTRACELLULAR (POTENTIAL).
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Best Local S
Matches 75
                 "Cloning and expression of the growth hormone/prolactin CELL 53:69-77(1988).
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CARBOHYD
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SEQUENCE
                                                                                                                             SEQUENCE OF 281-610 FROM N.A. BANVILLE D., STOCCO R., MURTI
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 91155946.
SHIROTA M., BANVILLE D., ALI S.,
EDERY M., DJIANE J., KELLY P.A.;
                                                                                                                                                                                                                                                                                                                                                                                              PRLR_RAT
P05710; Q63451;
Q1-NOV-1988 (RE)
                                                                                                                                                                                                          SEQUENCE FROM N.A. (LOI
STRAIN-SPRAGUE-DAWLEY;
                                                                BOUTIN J.-M.,
                                                                           EDLINE; 88165059.
                                                                                                                                                         HANG R., BUCZKO E., TSAI-MORRIS C.H., 
"Isolation and characterization of two 
receptor CDNA species"; 
BIOCHEM. BIOPHYS. RES. COMMUN. 168:415-
                                                                                                                                                                                                 EDLINE; 90241201
                                                                                                                                                                                                                                        MOL. ENDOCRINOL. 4:1136-1143(1990).
                                                                                                                                                                                                                                                                                                                                    EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                   21-NOV-1997
                                                                                     ISSUE-LIVER;
                                                                                                                   UBMITTED (MAR-1996)
                                                                                                                                                                                                                                                              Expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406
                                                                                             EQUENCE FROM N.A.;
                                                                                                                                                                                                                                                     iver.
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JS NORVEGICUS (RAT).
JS NORVEGICUS (RAT).
CHORDATA; VERTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YIVQIHCKP-----DHHGSWSEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPYLVLTW-SPPPLADVRSGWLTLDYELRLKPEEAEEWETI-FVGQQTHYKMFSLNPGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDQLSVRWVSPPALKDF----LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSCYFDKKHTSFWTIYNITYKATNEIGSNVSDPLYVDVTYIVQTDPPVNVTLELKKTVNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPEKPVNISCWSKNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YFVQVRCNPFGIYGSKKAGIWSEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDV--HVSRVGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPEKPTIIKCRSPEKETFTCWWKPGSDGG---HPTNYTLLYSKEGEERVYECPDYKTAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
75; Conserv
                                                                                                                                                                                                                                                                                                                                                          38 (REL. 09, CREATED)
37 (REL. 35, LAST SEQUENCE UPDATE)
97 (REL. 35, LAST ANNOTATION UPDATE)
RECEPTOR PRECURSOR (PRL-R) (LACTOGEN RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
263
304
316
336
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                                                                                                                                                                                                                                                             two
                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                      Q63723;
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263
304
316
336
94507
                                                                 JICOEUR C.,
                                                                                                                                                                                                                    (LONG
                                                                                                                                                                                                                                                            forms of
                                                                                             AND PARTIAL SEQUENCE
                                                                                                                 77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.5%;
                                                                                                                                                       COMMUN. 168:415-422(1990)
                                                                                                                                                                                                         NG FORM AND SHORT FORM).
TISSUE-OVARY;
                                            C., OKAMURA H., O
DUSANTER-FOURT
of the rat prola
                                                                                                                 MURTHY K.K., BOIE EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                     Q62832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW.
                                                                                                                                                                                                                                                            prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                 receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 316; DB
Pred. No. 1.6e
0; Mismatches
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POTENTIAL.
POTENTIAL.
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AE; MURINAE;
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                                                                                                                                                                                                                                                                                                                                                                                                     RT; 610 AA.
Q64274; Q63479;
                                                                                                                                                                                                                                                                                JOLICOEUR C.,
                                             prolactin
                                                                                                                                                                                                                                                            receptor
                                                                                                                                                                            HU Z.Z.,
                                          GAGNON J., EDERY M.
I., DJIANE J., KELI
actin receptor, a me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC32;
                                                                                             (MEDIUM FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
.6e-19;
                                                                                                                Y., KELLY P.A.;
DATA BANKS.
                                                                                                                                                                                                                                                                                                                                MAMMALIA; EUTHERIA;
                                   family.";
                                                                                                                                                                            rat ovarian
                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                BOUTIN
                                                                                                                                                                                      DUFAU M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                               J.M.,
                                            KELLY P.A.;
a member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 830;
                                                                                                                                                                            lactogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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SEQUENCE FROM N.A. TISSUE-LYMPHOMA;

(FORM NB2).

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CONFLICT
CONFLICT
                                                                                                                            VARSPLIC
VARSPLIC
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VARSPLIC
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DISULFID
CARBOHYD
                                                                                                                                                                                                                                     /ARSPLIC
                                                                                                                                                                                                                                                                    CARBOHYD
         EQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 92041834.

ALI S., PELLIGRINI I., KELLY P.A.;
"A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolactin receptor.";
J. BIOL. CHEM. 266:20110-20117(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MBL; M57668; G2063;
MBL; M34083; G2051;
MBL; L48060; G1019(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROSITE; PS00241; RECEPTOR_CYTOKINES_1; ROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 r send an email to license@isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prolactin receptors. Activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            se by non-profit institu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          etween the Swiss Institute of Bioinf
he European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Differential signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOL. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEAL K.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: DIFFERENT FORMS ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLICING OF THE PRLR GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95014432
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEMBRANE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ieration
                                    3411
345
345
465
541
                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YU-LEE L.Y.;
      Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A. (FORM NB2)
510
2339
465
466
5541
5541
5559
9
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                                                                                                                                                                                                                                                                                                                             610
117
222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transduction of the short, Nb2, and long Activation of interferon regulatory factor-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYCOPROTEIN; SIGNAL; REPEAT;
      ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is not removed.
                                                                                                                   MEDIUM FORM).
MISSING (IN MEDIUM FORM).
MISSING (IN FORM NB2).
                                                                                                                                                                                                                          EVKQLKDKKTYLWVKWSPPT -> DYRWEVSCHQEALPKSA
                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (BY SIMILARITY). FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                              KLN (IN SHORT FORM).
MISSING (IN SHORT FORM).
KGKSEELLSALGCQDFPPTSDCEDLLVEFL
IGSPSKYKVDLLYLALFGGFQKLDNAGELDY
                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                   PROLACTIN RECEPTOR.
                                                                          (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http:
                                                               REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions
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Best Local :
                                                                                                - POT -
                                                              ÷
                                                                                                                                                      SEQUENCE FROM N.A. (FORMS PRI-R2 AND PRL-R1).
STRAIN-SWISS WEBSTER; TISSUE-LIVER.
MEDLINE; 89261824.
DAVIS J.A., LINZER D.I.H.;
                                                                                                                                                                                                                                               SUBMITTED
                                                                                                                                                                                                                                                                                                                      SUBMITTED (JUL-1992) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (FORM PRL-R3).
                                                                                                                                                                                                                                                                                                                                                                                           ENDOCRINOLŌGY 133:224-232(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUS (MOUSE).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;

EUKARYOTA; MOTTERGRATHI; MURIDAE; MURINAE; MUS.
                                                                                                                          Expression of multiple forms of the iver.";
                                                                                                                                                                                                                                                                                STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 "Changes in prolactin receptor expression mouse ovary.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               LARKE D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SWISS WEBSTER; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and sequencing of the cDNA encoding the murine mammary gland long-form prolactin receptor."; SRNE 134:263-265(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOORE R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 94085788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C3H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRLR_MOUSE STANDARD;
Q08501; Q62099; P15213;
Q1-APR-1990 (REL. 14, CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROLACTIN RECEPTOR PRECURSOR (PRL-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDLINE; 93307149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A. (FORM PRL-R3).
TRAIN-C3H; TISSUE-MAMMARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 TOFKVFDLYPGQKYLVQTRCKP-----DHGYWSRWSQESSVEMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 RNLTL-EVKQLKDKKTYLMVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWE-IHFTGHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 POVHYSRYGGLEDQLSVRWY--SPPALKDF---LFQAKYQIRYRYEDSYDWKVVDDYSNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 NT--CEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVYTTDPP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 SLLKOQS-----PPGKPEIHKCRSPDKETFTCWWNPGTDGG--LPTNYSLTYSKE--GEK 65
                                . ENDOCRINOL. 3:674-680(1989).
FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROTACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: THREE FORMS, PRL-R1, PRL-R2 AND PRL-R3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 TYPECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYIVEPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 SILAGSCLYYGLPPEKPYNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSCRLAGLKPGTYYFYQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79;
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Similarity 35.0%;
                                                                                                                                                                                                                                   LB/C; TISSÜE-MAMMARY GLAND;
PEZET A., NANDI S., KELLY P.A.;
(JUN-1993) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REL. 14, CREATED)
(REL. 31, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OKA T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             LINZER D.I.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                         ARE PRODUCED
                                                                                                                                                                                                                                                                                         (FORM PRL-R3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FORM PRL-R3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P15212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 313; DB 1
Pred. No. 2e-19;
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                    ALTERNATIVE SPLICING
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                                                                                                                                                                                                                                                                                                                                                                                                                        pregnancy
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                  AND PRL-R3
OF THE PRLR
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SIMILARITY: BELONGS

TO THE CYTOKINE FAMILY OF RECEPTORS

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RESULT 5
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Best Local Similarity
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                             FTPYEIWVEATNRLGSARSDYLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVS--PP
                                                                                                                                                                                                                                         DKETFTCWWNPGSDGG--LPTNYSLTYSKE--GEKNTYECPDYKTSGPNSCFFSKQYTSI
                                                                                                                                                                                                                                                                   NMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNT--CEEYHTVGPHSCHIPKD-LAL
                                                                                                                                                                                                                                                                                              MSSALAYMLLVLSISLLNGQS----
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                                                                                                                                                    ALKDF --- LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 242
                                                                                                                                                                                WKIYIITVNATNEMGSSTSDPLYVDVTYIVEPEPPRNLTL-EVKQLKDKKTYLWVKWLPP
                                                                                                                                                                                                                                                                                                                       LSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSK 70
                                                                                                YGSKKAGIWSEWSHPTAASTP
                                                                     ----DHGYWSRWGQEKSIEIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00341; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT
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  STANDARD;
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                                                                     222
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                                                                                                                                                                                                                                                                                                                                                                Score 309.5; DB Pred. No. 4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (BY SIMILARITY).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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L -> F (IN REF. 2):
AA401E67 CRC32;
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MISSING (IN PRL-R2).
KGKSBELLSALGCQDbPPTSDCE -> LWCSILQLTSLVKI
PTIEELCDL (IN PRL-R1).
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  PRT;
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  831
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NSCYFDKKHTSFWTIYNITVRATNEMGSNSSDPHYVDVTYIVQPDPPVNVTLELKKPINR 346 HSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDV--HVSRVGGL

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01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, PRECURSOR (PRL-R) (CPRLP).
                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
SEQUENCE
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-WHITE LEGHORN; TISSUE-KIDNEY
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TANAKA M., MAEDA K.,
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Double antenna structure of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A
                                                        58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JQ1655;
                                         PPEKPVNISCWSKNMKDLICRWIPGAHGETFLH-TNYSLKYKLRWYGQDNTCEEYHTVGF 116
                                                                                                       Similarity 34.6
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A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLYCOPROTEIN;
                                                                                                                                                                                                                                                           MW;
                                                                                                             Score 308; DB Pred. No. 7.9e 28; Mismatches
                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
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POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
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     ---HPTNYTLLYSKEGEEQVYECPDYRTAGP
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                                                                                                 7.9e-19;
96;
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                                                                                                                Indels
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EMBL; U22947; G973165;
EMBL; U22924; G973166;
                                                                                                                               ISULFID
ARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as modified and this statement is not reentities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                             RANSMEM
                                                                                                                                                                                                                                                                                                                                                                ROSITE; PS00241; RECEPTOR_CYTOKINES_1; ROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PITTS G.R., YOU S.K., FOSTER D.N., EL HALAWANI M.E.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PISSUE-KIDNEY;
ZHOU J.F., ZADWORNY D.,
SUBMITTED (JUN-1996) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MELEAGRIS GALLOPAVO (COMMON TURKEY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; MELEAGRIDIDAE; MELEAGRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROLACTIN RECEPTOR PRECURSOR (PRL-R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-NOV-1997 (REL. 35, CREATED)
1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
5-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE OF 82-121 AND 473-522 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 YIIQIHCKP-----DHHGSWSEWSSENYIQIPNDFR 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 YFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSER 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -NOV-1997 (RE)
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                                                                                                                                                                                                                                                                                                            TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT
 228
326
35
75
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59
100
112
1132
262
303
315
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325
428
46
86
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110
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262
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315
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EMBL/GENBANK/DDBJ DATA BANKS
        POTENTIAL.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
POTENTIAL.
                                                                                                                                                                 FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III.
                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                           PROLACTIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                        OTENTIAL
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                                                                                                                                    SIMILARITY.
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PRLR_BOVIN
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                                                                                                                                           EMBL: L02549; G163618; -
PROSITE: PS00241; RECEPTOR_CYTOKINES_1;
PROSITE: PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                  SIGNAL
                                                                                                                                                                                                  modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                            PFAM; PF00041;
HSSP; P14787; 1
                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FALA:
BOS TAURUS (BOVINE).
BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE; BOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                               Molecular cloning of the bovine prolactin receptor and forciactin and growth hormone receptor transcripts in tero-placental tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                SCOTT P., KESSLER M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRLR_BOVIN
Q28172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROLACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 YFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTPRSER 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 KPYLMLTW-SPPPLADVRSGWLTLDYELRLKPEEGEEWETV-FVGQQTQYKNFSLNPGKK 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   287 NSCYFDRKHTSFWTVYNITVKATNEMGSNSSDPHYVDVTYIVOPDPPANVTLELKKPINR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
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                                                                                                                                                                                                                                                                                                                                                             CELL. ENDOCRINOL. 89:47-58(1992).
FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 PPEKPVNISCWSKNMKDLTCRWTPGAHGETFLH-TNYSLKYKLRWYGODNTCEEYHTVGP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDQLSVRWVSPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDV--HVSRVGGL
                                                                                                                           ; fn3; 2.
1AN3.
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                                                                                               GLYCOPROTEIN; SIGNAL; REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHULER L.A.;
 POTENTIAL.

CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III.

FIBRONECTIN TYPE-III.
                                                       EXTRACELLULAR (POTENTIAL)
                                                                         PROLACTIN RECEPTOR
                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
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Pred. No. 9.6e
26; Mismatches
                                                                                                                                                                                                            (See http://www.isb-sib
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).6e-19;
les 97;
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Best Local
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CARBOHYD
CARBOHYD
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Q28235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                 KELLY P.A., JABBOUR H.N.;
"Expression of the prolactin receptor gene during non-breeding seasons in red deer (Cervus elaphus): expression of two forms in the testis.";
J. ENDOCRINOL. 146:313-321(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CERVUS ELAPHUS (RED DEER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROLACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARTIODACTYLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   )1-NOV-1997 (REL.
01-NOV-1997 (REL.
15-JUL-1998 (REL.
PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PROSITE; PS00340; RECEPTOR_CYTOKINES_2; PFAM; PF00041; fn3; 2. HSSP; P14787; lan3.
                                                               EMBL; X94953; E218406;
                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                    CLARKE
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERVUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189
                                                                                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 --- DHGYWSEWSPESSIQIP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 YEIWVEATNRLGSARSDYLTLDILDVYTTDPPPDVHVSRVGGLEDQLSVRWV--SPPALK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 SRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNISCWSKN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 KETFTCWWEPGADGG--LPTNYTLTYHKEGETLIHECPDYKTGGPNSCYFSKKHTSIWKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72
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                                                                                                                                                                                                                              SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D----FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHI-PKDLALFTP
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                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               L.A.,
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nilarity 31.2%;
Conservative 3
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59
132
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X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9,4,6
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132
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE
                                                                                                                                                                                                                                                                                                                                                                                                   LOUDON A.S., RANDALL V.A., POSTEL-VINAY M.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263
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Pred. No. 6.8e-1
B; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                    (Cervus elaphus):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CERVOIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      581 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UPDATE)
                                                                                                                                                  There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MMALIA; EUTHERIA;
CERVIDAE; CERVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                       PITUITARY HORMONE
                                                                                                                                                                  restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CERVINAE;
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CCCCCCRATAX RAPRET RAPER RAPE
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Best Local S
Matches 75
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CARBOHYD
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SEQUENCE
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DOMAIN
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TRANSMEM
                                                                                                                                                                                                                                                                                                                 P1478/;
01-APR-1990 (REL. 14, CREATEU)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                          _RABIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                               receptor.";
PROTEINS 27:459-468(1997).
-I- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR
                                                                                                                                                                                                                                                                          ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
                                                                                                                                                                                                                            TISSUE-MAMMARY GLAND;
MEDLINE; 89184578.
                                                                                                                                                                                                                                                                                                                                                                     P14787;
                                                                                                                                                                                                                                                                                                                                                                              PRLR_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 QDNTCEEYHTVGPHSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPP
                                                                                                                       3D-STRUCTURE MODELLING OF MEDLINE; 97248733.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131
                                                                                                              HALABY D.,
                                                                                                                                                                    receptor by molecular nammary gland.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       189
                                                                                                                                                                                                                                                                                                                                                                                                                                                           218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
                                                                                                 ALABY D., THOREAU Homology modeling
                                                                                                                                                                             DERY M., JOLICOEUR C., LEVI-MEYRUEIS C., ETRIDOU B., BOUTIN J.M., LESUEUR L., KELI Identification and sequence analysis of eceptor by molecular cloning of complements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18. NASLLNGQS-----PPGKPKIIKCRSPGKETFTCWWEPGSDGG--LPTNYTLTYHKEGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 DGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71
                 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIHECPDYKTGGPNTCYFSKKHTSIWKIYVITVNAINQMGVSSSDPLYVDVTYIVEPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDVHVSRVGGLEDQLSVRWVS--PPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       TQLKIFSLYPGQKYLVQVRCKP-----DHGYWSEWSPESSIQIP
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                                                                                                    rabbit
                                                                                                              DJIANE J.,
                                                                                                                                                          U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ME:
                                                                                                                                     30-228
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BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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Pred. No. 1.1e-18;
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                                                                                                   g J., MORNON J.P.;
prolactin hormone
                                                                                                                                                           86:2112-2116(1989).
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                 complementary DNA
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                                                                                                                                                                                            C., DUSANTER-FOURT
KELLY P.A., DJIANE
of a second form of
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                                                                     PITUITARY HORMONE
                                                                                                                                                                                   from
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                                                                                                                                                                                                                                                                                        EUTHERIA;
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Query Match
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                                         STRAIN-ICR; TISSUE-MACROPHAGE;
MEDLINE; 92291532
SAITO M., YOSHIDA K., HIBI M., TAGA T., KISHIMOTO T.;
"MOLECULAR CLONING Of a murine IL-6 receptor-associated transducer, gpl30, and its regulated expression in vivo.
J. IMMUNOL. 148.4066-4071(1992)
                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                           11-FEB-1995 (REL. 31, CREATED)
11-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                ODENTIA; SCIUROGNATHI; MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 LVQVRCKP-----DHGFWSVWSPESSIQIP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 FYOVRCNPFGIYGSKKAGIWSEWSHPTAASTP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                             SUOW_89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 PPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPH 117
 FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE FILE-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPYLWYKWLPPTLVDVRSGWLTLQYEIRLKPEKAAEWE-THFAGQQTQFKILSLYPGQKY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSVRWVS--PPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCYFSKKHTSIWTIYIITVNATNQMGSSVSDPRYVDVTYIVEPDPPVNLTL-EVKHPEDR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHI-PKDLALFTPYEIWYEATNRLGSARSDVLTLDILDVYTTDPPPDVHYSRVGGLEDQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPGKPFIFKCRSPEKETFTCWWRPGADGG--LPTNYTLTYHKEGETITHECPDYKTGGPN 84
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75; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 300.5; DB 1;
Pred. No. 2.4e-18;
9; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                MURINAE;
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THE RECEPTOR SYSTEMS FOR ILIZE GP130 FOR INITIATING
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DISULFID
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122 PKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRW 181
                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
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                                         130 TNITCIVNEGKNMLCOMDEGR--ETYLETNYTLKSE--WATEKFEDCOSKHGT---SCMV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                63 VNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGOD-NTCEEYHTVGPHSCHI 121
                                                                                                                         70 NHAAVPREQVTVINRTTSSVTFTDVVLPSVQLTCNILSFGQIEQNVYGVTMLSGFPPDKP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GD; MGI:96560; IL6ST.
ROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
                                                                                                                                                                     3 NGRRLPPELSRVLNASTLALALANLNGSRORSGDNLVCHARDGSILAGSCLYVGLPPEKP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 OF GESTATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINE DURING THE REST OF EMBRYOGENESIS.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE IG-LIKE DOMAIN.

SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS, SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED EXCEPT BAF-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
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                                                                                                                                                                                                                           83;
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                             917 AA;
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                    15.5%;
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                                                                                                                                                                                                                                                                                                                         102452 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, HE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
                                                                                                                                                                                                                                        Score 297; DB
Pred. No. 7.8e-
                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                   124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECEPTOR BETA CHAIN (POTENTIAL).
                                                                                                                                                                                                                                                        Length 917;
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P40189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 11
HUMAN
                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Crystal structure of a cytokine-binding EMBO J. 17:1665-1674(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91084844.
HIBI M., MURAKAMI M.,
                                                                                                        EMBL; M57230; G186354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gp130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
           PROSITE; PS00340; RECEPTOR_CYTOKINES_2; PFAM; PF00041; fn3; 3. RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 9816938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
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ISSUE-MYELOMA, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
5-DEC-1998 (REL. 37, LAST ANOTATION UPDATE)
NTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (
SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 1
ECEPTOR) (CDW130) (CD130 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-FEB-1995
                                                                                                                                       send
                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: SIGNAL TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GR130 FOR INITARING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES, AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IL EMBRYONIC DEVELOPMENT (BY SIMILARITY). SUBCRETIONER OF AN ALPHA AND A BETA CHAIN. SUBCRELIULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES. EXAMINED. EXPRESSION NOT RESTRICTED TO IL-6 RESPONSIVE CELLS. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
                                                                         ; A36337;
; 1BQU; 20
                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS. DATABASE: NAME-PROW; NOTE-CD guide CD130 entry:
                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
ONE IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                  WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cdl30.htm".
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                                                            600694
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                                                                                                                                       20
           TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD;
                                                                         26-AUG-98
                                                                                                                                       email to license@isb-sib.ch).
                                                                                           A36337
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AE; HOMO.
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region of gpl30.";
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130) (GP130)
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             SIGNAL;
                                                                                                                                                                                                                    outstation
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Best Local S
Matches 76
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SEQUENCE
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DISULFID
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DOMAIN
                                                                                                         01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
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918
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131
157
227
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383
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28.7%;
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INTERLEUKIN-6 RECEPTOR BI
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASNIC (POTENTIAL).
IG-LIKE CZ-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
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POTENTIAL.
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POTENTIAL.
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Pred. No. 2.
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7CC06F05 CRC32;
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7;

TISSUE-LIVER;

MEDLINE; 93052397.

WANG Y., BESBITT J.E., FUENTES N.L., FUI

"Molecular cloning and characterization

transducing molecule, gpl30.";

GENOMICS 14:666-672(1992).

FULLER of.

R G.N

rat liver IL-6 signal

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RATTUS NORVEGICUS (RAT). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;

MAMMALIA; EUTHERIA; RATTUS.

SEQUENCE FROM N.A.

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                                                     126
                                                                                               134
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             188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR IL-6, LLF, COM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BUNDING SITES, AND TRANSDUCES THE SIGNAL DOES NOT BIND IL-6. MAY HAVE A ROLE IN EMBRYONIC DEVELOPMENT (BY SIMILARITY).

SUBUNIT: HETERODIAGR OF AN ALPHA AND A BETA CHAIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                          ALFTPYEIWVEATURIGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPP 185
                                                                                                                                                                                                               LPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLPPEKPVNIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                                                                               CWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQD-NTCEEYHTVGPHSCHIPKDL 125
IYFVNIEVWVEAENALGNVSSEPINFDPVDKVKPSPPHNLSVTNSEELSSILKLAWVNSG 247
                                                                                    CIVNEGKNMLCQLDPGR--ETYLETNYTLKSE--WATEKFPDCRTKH--GTSSCMMGYTP 187
                                                                                                                                                                       VPKEQVTVINRTASSVTFTDVVFQNVQLTCNILSFGQIEQNVYGITILSGYPPDIPTNLS 133
                                                                                                                                                                                                                                                                     81;
                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENDOTHELIAL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A44257
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A
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                                                                                                                                                                                                                                                                                    14.98;
                                                                                                                                                                                                                                                                                                                                                                           102450 MW;
                                                                                                                                                                                                                                                       Score 285; DB 1; I
Pred. No. 8.4e-17;
6; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERLEUKIN-6 RECEPTOR BETA CHAIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIBRONECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                       E6EDFCD0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE-III.
                                                                                                                                                                                                                                                                                                    Length 918;
                                                                                                                                                                                                                                                              Indels
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      Matches
                        Query Match
Best Local
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                        DOMAIN
DOMAIN
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TELEOSTEI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _ORENI
                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fcentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restricte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L34783; G903847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SANDRA O., SOHM F., DE LUZE A., PRUNET P., EDERY M., KELLY P.A.; "EXPRESSION Cloning of a CDNA encoding a fish prolactin receptor."; PROC. NATL. ACAD. SCI. U.S.A. 92:6037-6041(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORBOCHROMIS NILOTICUS (NILE TILAPIA) (TILAPIA NILOTICA).
EUKARYOTA: METAZOA; CHONDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
TELEOSTEI: EUTELEOSTEI; ACANTHOPTERYGII; PERCOMORPHA; PERCIFORMES;
LABROIDEI; CICHLIDAE; TILAPIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRLR_ORENI
Q91513;
                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDLINE; 95320210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 ALKDFLFQAKYQIRYRVEDSVDWKVV---DDVSNQTSCRLAGLKPGTVYFVQVRCNPFGI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 KENGK-GYWSDWSE-EASGTTYEDRP 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 YGSKKAGIWSEWSHPTAASTPRSERP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 L--DSILRLKSDIQYRTKDASTWIQVPLEDTVSPRTSFTVQDLKPFTEYVFRIR----SI
                          Similarity
                                                                                                                                                                                                                                                                                                                                                 TRANSMEMBRANE;
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REL. 35, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
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                        13.7%;
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                                                                                                                                                                                                                                                                                                                                           GLYCOPROTEIN; SIGNAL; REPEAT
                                                                                                     ¥.
      27;
Score 263.5; DB 1;
Pred. No. 3.7e-15;
7; Mismatches 94;
                                                                                                 POTENTIAL.
POTENTIAL.
E9A4E553 CRC32;
                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                 EXTRACELLULAR
                                                                                                                                                                                                                                                                                                          PROLACTIN
                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                       Length
Indels
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                                         630;
23;
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Gaps
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CHIPKDLAL-FTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQ- 177 PGKPTEIKCRSPEKETFTCWWKPGSDGG---LPTTYALYYKKEGSDVVHECPDYHTAGKNS PERPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHS 118

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MEDLINE: 90235283.

FUKUNAGA R., ISHIZAKA-IKEDA E
"Expression cloning of a rece;
stimulating factor.";
CELL 61:341-350(1990).
                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSEGR.
CSEGR.
USCULUS (MOUSE).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUKARYOTA; MURIDAE; MURIDAE; MURIDAE;
 TRANSMEM
                                                                                                                                                                     EMBE; M58288; G193455; -. PIR; A34898; A34898.
             DOMAIN
                                                   SIGNAL
                                                                REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          motif of the granulocyte colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAMASAKI K., NAITO S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCSR_MOUSE
P40223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAT. STRUCT. BIOL. 4:498-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Solution structure of an extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 225-333.
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                                                                                                                                                                                                                                                                                                                                               SUBUNIT: DIMER (PROBABLE).
SUBCELLULAR LOCATION: TYPE I
TISSUE SPECIFICITY: FOUND IN
SIMILARITY: BELONGS TO THE IN
                                                                                                                                                                                                                                                                                                                  ONE IG-LIKE DOMAIN.
SIMILARITY: CONTAIN
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                        STRUCT. BIOL. 4:498-504(1997).
FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR.
ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION EVEN
THE CELL SURFACE.
                                                                                                                             MGI:88533; CSFGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPFLRVSW-EPPRKADTRSGWITLIYELRVKLEDEESEWE-NHAAGQQKMFNIFSLRSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LSVRWVSPPALKDF---LFQAKYQIRYRVED-SVDWKVVDDVSNQTSCRLAGLKPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CFFNKNNTLIWVSYNITVVATNALGKTYSDPQDIDVVYIVQPHPPEKLEVT---VMKDQG
                                                                                                                                                                                                       s requires a license agreement (See http://www.isb-sib.ch/announce, an email to license@isb-sib.ch).
                                                                                                  PS00340; RECEPTOR_CYTOKINES_1; PS00340; RECEPTOR_CYTOKINES_2;
                                                                           TRANSMEMBRANE;
                                                                -STRUCTURE
                                                                                                                                           22-OCT-97.
22-OCT-97.
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627
                                                                                          fn3;
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                                                                                                                                                                                                                                                                                                                BELONGS
                                                                                                                                                                                                                                                                                                            CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS. BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                         GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor
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                                   POTENTIAL.
GRANULOCYTE COLONY STIMULATING
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                        RECEPTOR.
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BONE MARROW.
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                                                                         IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTA Y.;
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                                                                        SIGNAL;
                                    FACTOR
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SEQUENCE
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 381
                               342
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                                                                                                                                          108
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              KSHKTRNQH---RTRGSC
                                                                                                        ----PDVHVSRVGGLEDQLSVRWVS-PPALKDFLFQAKYQIRYRVE-DSVDWKVVDDV-S
                                                                                                                                                                     LYVGLPPEKPVNISC-WSKNMKDLTCRWTPGAHGETFLHTNYSLK-YKLR---WYGQDNT
PDHOGODIHLCNTTQLSC
                                          PGGGACEPRGGEPSS------GPVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAWMQ
                              ----WCQKKQLDPGTVSVQLFWKPTPLQEDSGQIQGYL-
                                                                         NQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWS-----HPT-AASTPRSERPG
                                                                                           LDIGPDVVSHQPGCL-----
                                                                                                                       PDCVAKKRQNNCSIPRKNLLLYQYMAIWVQAENMLGSSESPKLCLDPMDVVKLEPPMLQA
                                                                                                                                      CEEYHTVGPHSCHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPP----
                                                           SKDQFELCGLHQAPYYTLQMRC----IRSSLPGFWSPWSPGLQLRPTMKAPTIRLDT--
                                                                                                                                                      LHAGYPPASPSNLSCLMHLTTNSLVCQWEPGP--ETHLPTSFILKSFRSRADCQYQGDTI
                                                                                                                                                                                       , 68
                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                          12.6%;
398
               : 335
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                                                                                                                                                                                      45;
                                                                                          WLSWKPWKPSEYMEQECELRYQPQLKGANWTLVFHLPS
                                                                                                                                                                                                                                                                                                                                           IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                           POTENTIAL.
D55F84D4
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Pred.
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POTENTIAL.
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                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                     SIMILARITY.
                                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                             241;
No. 4
                                                                                                                                                                                                                            CRC32;
                                                                                                                                                                                            DB 1;
.5e-13;
                                                                                                                                                                                      112;
                                                                                                                                                                                                    Length
                                                                                                                                                                                     Indels
                                                                                                                                                                                                    837;
                                                                                                                                                                                    72;
                             SNMST
                                                                                                                                                                                    Gaps
                                           320
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                                                           342
                                                                          269
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                                                                                          288
                                                                                                                                       163
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AC COC COL DIT
                                                                                                                                                                                                       CNTR_RAT
                                                                                                                                                                                                                    RESULT
                                                                                                                                008406;
01-FEB-1995 (REL. 31, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CILLARY NEUROTROPHIC FACTOR RECEPTOR ALPHA PRECURSOR
                 MEDLINE; 93152175.

IP N.Y., MCCLAIN J., BARREZUETA N.
WIEGAND S.J., FRIEDMAN B., DAVIS S
"The alpha component of the CNTF r
                                                                                                      RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                              CNTR_RAT
                                                              TISSUE-BRAIN;
                                                                       SEQUENCE FROM
                                                                                             RODENTIA;
                                                                                                                                                                                                                  15
         defines
                                                                                             SCIUROGNATHI;
      potential
                                                                       N.A.
                                                                                                                                                                                            STANDARD;
                the CNTF
                                                                                           MURIDAE;
      targets
                                                                                          VERTEBRATA;
AE; MURINAE;
SS., i... IF receptor i
                                                                                                                                                                                            PRT;
                          X., ALDRICH T.H.,
S., YANCOPOULOS G.
                                                                                                                                                                                            372
                                                                                          MAMMALIA;
RATTUS.
                                                                                                                                                                                            ⋛
     is required for adult and during
      during
                                    PAN L.,
                                                                                                                                    (CNTFR ALPHA).
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Query Match
Best Local Similarity
Matches 90; Conserv
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216 PSNPRRLEVTWQTPSTWPDPESFPLKFFLRYRPLILDQWQHV-ELSNGTAHTITDAYAGK 274
                                       171 GGLEDQLSVRWVSPPALKD-FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGT 229
                                                                                 159 AL-KNRCHI-RYMHLFSTIKYKVSISVSNALGH-NTTAITFDEFTIVKPDPPENVVARPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARBOHYD
ARBOHYD
ARBOHYD
ARBOHYD
                                                                                                             113 TVGPHSCHIPKDLALFT--PYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRV 170
                                                                                                                                                                  111 EPV-LSCRSNTYPKGFYCSWHLSAPTYIPNTFNVTVLHGSKMM------VCEKDP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; S54212; G265056;
EMBL; S57711; G299332;
PIR; A47387; A47387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLATTERBUCK R.E., PRICE D.L., KOLIATSOS V.E.;
"Ciliary neurotrophic factor prevents retrograde neuronal death in the adult central nervous system.";
PROC. NATL. ACAD. SCI. U.S.A. 90:2222-2226(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 185-277 FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
                                                                                                                                                                                                           61 KPVNISCWSKNM-KDLTCRW-----TPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  odified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       development.";
NEURON 10:89-102(1993).
                                                                                                                                                                                                                                                   59 VNGTDLAPDL---LNGSQLILRSLELGHS-----GLYACFHRDSWHLRHQVLLHVGLPPR 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     he European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROSITE; PS00241; RECEPTOR_CYTOKINES_1; FALSE_NEG
                                                                                                                                                                                                                                                                                            2 LNGRRLPPELSRVINASTLALALANINGSRQRSGDNIVCHARDGSILAGS-CLYYGLPPE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HETEROTRINER OF THE ALPHA CHAIN, LIFR AND GP130.
SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
TISSUE SPECIFICITY: NERVOUS SYSTEM.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION:
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDS TO CNTF (GPA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN. BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          40822 MW;
                                                                                                                                                                                                                                                                                                                                        11.8%; Score 226.5; DB 1; 28.4%; Pred. No. 2.9e-12; tive 34; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    institutions as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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GPA). THE ALPHA CHAIN PROVIDES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PI-ANCHOR (POTENTIAL).
-> D (IN REF. 2).
B63000CA CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             its content
                                                                                                                                                                                                                                                                                                                                                                                    Length 372;
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Search completed: September 17, 1999, 03:10:14
Job time: 294 sec

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Result
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Perfect score:
Sequence:
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                                                                                                                                                              325.5
309.5
306.5
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1919
1 TLNGRRLPPELSRVLNASTL.....TRGSCPRADGARREVLPDKL 350
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sp_phage:*
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sp_unclassified:*
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                                                                                O88507 mus musculu
O99665 homo sapien
O64385 mus musculu
O16542 homo sapien
p70225 mus musculu
p97378 mus musculu
O57320 xenopus lae
                                                                                                                                                                               075462 homo sapien
057519 xenopus lae
016354 homo sapien
046561 ovis aries
018880 bos taurus
093404 oreochromis
046386 mustela vis
018985 cervus elap
079203 ovis aries
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343 mus musculu
960 rattus norv
20 homo sapien
21 homo sapien
                                                                       rattus norv
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01-JUN-1998
01-MAY-1999
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057519;
                                                                                         MEDLINE;
FUH G., W
                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
PFAM;
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Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHEN J.,
               ğ
                           PFAM;
                                                cancer cell lines.";
J. Biol. Chem. 270:13133-13137(1995).
                                                                                                                                                        Homo sapiens (Human
Eukaryota; Metazoa;
                                                                           Prolactin receptor antagonists
                                                                                                                                                                                  PROLACTIN RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                       231
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bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
satrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                       EQUENCE FROM N.A
EDLINE; 95286597
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                                                                                                                                                                                                                                                                                                                                                                        PNALKIEWKNPIT - -
                                                                                                                                                                                                                                                                                                                                                                                              EDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVV---DDVSNQTSCRLAGLKPGTV 230
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                                     ol. Chem. 270:13133-
S78505; AAB34470.1;
                          PF00041;
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91; Conservative
                                                                                         WELLS J.A.;
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 206
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                                                                                                                                                                   (Human)
                          fn3;
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                                                                                                                                                       Chordata; Craniata;
                                                                                                                                          Catarrhini;
 23950
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Last sequence up
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9; Mismatches
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D7E57266 CRC32;
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4.7e-22;
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Xenopodinae;
                                                                          of breast
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Best Local
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Best Local
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                                                                                                                                                                                                              SEQUENCE
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Submitted (JAN-1998) 1
EMBL; AF041257; AAB96:
PFAM; PF00041; fn3; 2
                                                                                                                                                                                                                                                                                                                                     "Long and short forms of the ovine prolactin receptor: cDNA cloning genomic analysis reveal that the two forms arise by different alternative splicing mechanisms in ruminants and in rodents.";
J. Mol. Endocrinol. 19:109-120(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrembLrel.
01-JUN-1998 (TrembLrel.
01-MAY-1999 (TrembLrel.
PROLACTIN RECEPTOR LONG
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 98001468.
BIGNON C., BINART N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Eutheria; Cetartiodactyla; Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
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                                                                                                                                                                                                                                                                                                   BIGNON C.
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                  41
                                                                                                                      12 SRYLNASTLALALANLNGSRQRSGDNLYCHARDGSILAGSCLYYGLPPEKPYNISCWSKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 NSCHFGKQYTSMWRTYIMWVNATNQMGSSFSDELYVDVTYIVQPDPPLELAV-EVKQPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 LPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGP
                                                                       72 MKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHIPKD-LALFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                7 SRVLFILLTELFASLINGQS--
                       YEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWV--SPPALK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLSVRWV--SPPALKDF---LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTV
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YVITVSAINOMGISSSDPLYVDVTYIVEPEPPVNLTL-ELKHPEDRKPYLWIKWSPPTLT
                                                KETFTCWWEPGADGG--LPTNYTLTYRKEGETLIHECPDYKTGGPNSCYFSKKYTSIWKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWE
                                                                                                                                                  83;
                                                                                                                                                              Similarity
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06, Last sequence update)
10, Last annotation updat
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                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                            Score
Pred.
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PROLACTIN RECEPTOR

6792A7C7 CRC32;
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Pred. No. 1e
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                                                                                                                                                  Mismatches
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                                                                                                                                                            309.5;
No. 1.2
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157
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DF --- LFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGS

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Best Local
                                                        Oreochromis mossambicus (Mozambique tilapia) (Tilapia
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; A
Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
Perciformes; Labroidei; Cichlidae; Tilapia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHULER L.A., NAGEL R.J., GAO J., Prolactin receptor heterogeneity
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TIEMBLITEL 05, Creat
01-JAN-1998 (TIEMBLITEL 05, Last
01-NOV-1998 (TIEMBLITEL 08, Last
PROLACTIN RECEPTOR SHORT FORM.
                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           158
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                                                                                                                                                                                                                                                                                                                                                                                                                                   131
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EMBL; AF027403; AAB83999.1; -.
PFAM; PF00041; fn3; 2.
SEQUENCE 296 AA; 33854 MW; 8B4
                                                                                                                        1-NOV-1998 (TrEMBLIEL 08, C:
1-NOV-1998 (TrEMBLIEL 08, L:
1-MAY-1999 (TrEMBLIEL 10, L:
ROLACTIN RECEPTOR (FRAGMENT)
                                                                                                                                                                                                                                                                              211 --- DHGYWSEWSPESSIQIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 DVKSGWFSIQYEIRLKPEKATDWE-THFAPKLTQLKIFNLYPGQKYLVQIRCKP---
                                                                                                                                                                                                                                                                                                                              DVKSGWFIIQ--YEIRLKPEKATDWE-THFTLKQTQLKIFNLYPGQKYLVQIRCKP----
                                                                                                                                                                                                                                                                                                                                                                                           YVITVNAINQMGISSSDPLYVHVTYIVEPEPPANLTL-ELKHPEDRKPYLWIKWSPPTMT 157
                                                                                                                                                                                                                                                                                                                                                                                                                        YEIWVEATURLGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWV--SPPALK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                       KETFTCWWEPGADGG--LPTNYTLTYHKEGETLIHECPDYKTGGPNSCYFSKKHTSIWKM
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                                                                                                                                                                                                                                                                                                        GSKKAGIWSEWSHPTAASTP 263
                                                                                                                                                                                                                                                                                                                                                            D-----FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIY 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHI-PKDLALFTP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -DHGYWSEWSPESFIQIP
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08, Last sequence update)
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 MORI T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 306.5; DB 6;
Pred. No. 9.4e-21;
8; Mismatches 94;
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TETSUYA H.;
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                                                                                                                                     update)
                                                                                                  (Tilapia
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Best Local Similarity
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Best Local :
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NON_TER
SEQUENCE
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 255
                                                            195
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01-JUN-1998 (TIEMBLIE1. 06, Last sequence update)
01-MAY-1999 (TIEMBLIE1. 10, Last annotation update)
PROLACTIN RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        046386
                              119
                                                                                                         140 RIGSARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVS--PPALKDF---LFQA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mustela vison (American mink).
Eukaryota; Metazoa; Chordata; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           046386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-1998) to the EMBL; AF080247; AAC31825.1; PFAM; PF00041; fn3; 2; NON_TER 346 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sutheria; Carnivora;
                                                                                                                                                                  81 PGAHGETFLHTNYSLKYKLRWYGQDNTCEEYHTVGPHSCHI-PKDLALFTPYEIWVEAIN 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 TYLIQVRCKP-----DHGFWSEWSSTSYVKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 VYFVQVRCNPFGIYGSKKAGIWSEWSHPTAASTP 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 WPFLRVSW-EPPHRADTRSGWITLIYELRVKLEDEESEWE-NHAAGQQKMFNIFSLRSGG
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                                                                                         60
                                                                                                                                         2 PGEDGG--LPTKYTLTYHKEGETTTHECPDYITSGPNSCYFNKKHTSIWTMYIITINATN
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                                                                                                                                                                                                                                                                                                                                                                                       SSUE-TESTIS;
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                                                 KYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEW
                                                                                EMGSSSSDPRYVTLTYIVEPDPPVNLSL-ELKQPEDKKTYLWIKWYPPTLVDVRSGWLTL
SHPTAASTP 263
                       QYEIRLKPEKATEWE-THFAGLQTQFKILSLYPGQKYLVQVRCKP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---LSVRWVSPPALKDF---LFQAKYQIRYRVED-SVDWKVVDDVSNQTSCRLAGLKPGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGRPTEITCRSPEKETFTCWWKPGSDGG--LPTTYALYYRKEGSDVVHECPDYHTAGKNS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEXPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYGODNTCEEYHTVGPHS 118
                                                                                                                                                                                                          61;
                                                                                                                                                                                                                                                                                 217
217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 AA;
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                 24850 MW;
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                                                                                                                                                                                                                                                                                                                                                                      HOUDE A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 270.5;
Pred. No. 2.5e
                                                                                                                                                                                                     Score 235.5; DB 6
Pred. No. 2.4e-14;
0; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Mammalia;
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                                                                                                                                                                                                                                                                              F77A3B9D CRC32;
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TIEMBLIE). 03, Created)
01-MAY-1997 (TIEMBLIE). 03, Last sequence update)
01-NOY-1998 (TIEMBLIE). 08, Last annotation update
PROLACTIN RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-1997) to t) EMBL; Y14753; CAA75048.1; PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                  STRAIN-M22/80; TISSUE-ANTERIOR PITUITARY;
TORTONESE D.T., BROOKS J., INCLETON P., MCNEII
SUBMITTED (JAN-1997) to the EMBL/GenBank/DDBJ
EMBL; Y105/8; CAA71597.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cervus elaphus nelsoni (American elk).
Eukaryota; Metazoa; Chordata; Craniata
Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                   PFAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sutheria; Cetartiodactyla;
Servinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       aprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 TSSR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 TSCR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 ANLTL-ELKHPEDRKPYLWIKWFPPTLTDVKSGWFMIQYEIRLKPETATDWE-HDDLHPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163
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85 GETFLHTNYSLKYKLRWYGODNTCEEYHTVGPHSCHIPKD-LALFTPYEIWVEATNRLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-JAN-1998
1-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 DGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYKLRWYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDNTCEEYHTVGPHSCHI-PKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPP
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                                                                                                                                                                                                                                                PF00041;
                                                   1 Similarity
57; Conser
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335 AA;
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198 AA;
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(TrembLrel. 05, Last sequence update)
(TrembLrel. 08, Last annotation updat
                                                   Conservative
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                                                                                                                                                                                                                                                fn3; 1
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38326
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                                                                     11.8%;
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                                              Score 225.5;
Pred. No. 3.5e
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 231.5; DB Pred. No. 5e-14;
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                                                                  225.5; DB
No. 3.5e-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Pecora; Bovoidea; Bovidae;
                                                                                                                                                                      CRC32;
                                                                                                                                                                                                                                                                                         MCNEILLY A.S.;
k/DDBJ databases
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                                                68;
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                                              31;
                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSUE-BRAIN, SKELETAL MUSCLE; MAKDA M., YAGUCHI N., HANYUU C., NAKATA Y., ONODA N., TU KADDAM M., KIKUCHI Y., NOMURA H.; KOJIMA T., HASEGAMA M., KIKUCHI Y., NOMURA H.; Mouse homolog of human cillary neurotrophic factor recessible to the EMBL/GenBank/DDBJ databases. EMBL; AF068615; AAC25711.1; -. PFAM; PF00041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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Eukaryota; Metazoa; Chordata;
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     329
                                                    269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 AASTP
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  PPTTKICDPGELGSGGGPS
                                               GPGGGACEP----RGGEPS
                                                                                                                                                                                                                                                               GGLEDQLSVRWVSPPALKD-FLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGT
                                                                                                                                                                                                                                                                                                                   AL-KNRCHI-RYMHLFSTIKYKVSISVSNÄLGH-NTTAITFDEFTIVKPDPPENVVARPV
                                                                                                                                                                                                                                                                                                                                                                     TVGPHSCHIPKDLALFT--PYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPVNISCWSKNM-KDLTCRW-----TPGAHGETFLHTNYSLKYKLRWYGQDNTCEEYH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNGTDLAPDL --
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                                                                                                   EYIIQVAAK-----DNEIGTWSDWSVAAHATPWTEEPRHLTTEAQAPETTTSTTSSLAP
                                                                                                                                                        VYFVQVRCNPFGIYGSKKAGIWSEWS---
                                                                                                                                                                                                             PSNPRRLEVTWQTPSTWPDPESFPLKFFLRYRPLILDQWQHV-ELSDGTAHTITDAYAGK
                                                                                                                                                                                                                                                                                                                                                                                                                             EPV-LSCRSNTYPKGFYCSWHLPTPTYIPNTFNVTVLHGSKIM------VCEKDP
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Sciurognathi; Murida
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CILIARY NEUROTROPHIC
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No. 2.2
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ae; Murinae;
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Best Local
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
INTERLEUKIN-1 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1)
                                    SEQUENCE FROM N.A
                                                             HALTON D.J., HILTON A.A., RAICEVIC A., RAKAR S., HARRISON-SMITH M., GOUGH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILLSON T.A.; "Cloning of a murine II-11 receptor alpha-chain; requirement for gpl30 for high affinity binding and signal transduction."; EMBO J. 13:4765-4775(1994):
                                                                                                                                                                                                          Q64385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRESKY D.H., YANG H., MINI GATELY M.K., GUBLER U.; Submitted (JUL-1996) to the EMBL; U64198; AAB36675.1;
                                                                                                                                           EDLINE; 95045367
                                                                                                                                                                                                                                                                                                                                                                                                                                       318 EEEPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                         EQUENCE FROM N.A.
                                                                                                                                                                                                                                            Llirai or illira or etl2 or et12/Illi rec
                                                                                                                                                                                                                                                                 IL-11RALPHA) (IL11RA1)
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1-MAY-1997 (TrEMBLrel. 03,
1-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSRLWNMVNVTKAKGRHDLLDLKPFTEYEFQI-SSKLHLY----KGSWSDWSESLRAQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPFGTYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARSDVLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y----KLRWYGQ--DNTCEEYHTVG-----PHSCHIPKDLALFTPYEIWVEATNRLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMK-DLTCRWTPGAHGETFLHTNYSLK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSSLPSTFTFLDIVRPLPPWDIRIKFQKASVSRCTLYW-----
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       Ξ.
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 /C, AND C57BL/6; TISSUE-EMBRYO; BETTENHAUSEN B., BILINSKI P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          862 AA;
                                                                                                                                                         /6 X CBA;
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                  Sciurognathi; Muridae; Murinae;
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                                                                                                                                                       TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MINETTI L.J., CHUA A.O., NABAVI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
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Last annotation update)
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Pred. No. 5.4e-11;
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                                                                                                                                                                                                              Craniata; Vertebrata;
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SIMON-CHAZOTTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -RDEGLVLLNRLRYRPS
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CARBOHYD
SEQUENCE
      Q16542
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EMBL; X94163; CAA63873.
MGD; MGI:107426; IL11RA
                                                                                                                                        265
                                                                                                                                                                      205
                                                                                                                                                                                                                                                   150 KKTLPGAESQRESPSTGPWPC--PQDPLEASRCVVHGAEFWSEYRINVTEVNPLG-ASTC
                                                                                                                                                                                                                                148
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Dev. Biol. 166:521-542(1994).
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alochem. J. 320:359-363(1996)
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                                                                                                                                                                                                                                                                               99 LRWYGQDNTCEEYHTVGPHSCHIPKD------LALFTPYEIWVEATNRLGSARSD 147
                                                                                                                                                                                                                                                                                                               93 VCQTLDGVSGGMVTLKLGFPPARP-EVSCQAVDYENFSCTWSPGO--VSGLPTRYLTSYR 149
                                                                                                                                                                                                                                                                                                                                             39 VCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Two differentially expressed interleukin-11 receptor genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C, AND C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILINSKI P., HALL M.A., NEUHAUS H., GISSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA C. TISSUE SPECIFICITY: WIDELY EXPRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS
                                                                                                  PRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKH 301
                                                                                                                                HPANSTVEPIGLEEVITDAVAGLP----HAVRVSARDF----LDAGTWSAWS-PEA---
                                                                                                                                                           SVDWKVVDDVSNQ--TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAST
                                                                                                                                                                                         LLDVRLQSILRPDPPQGLRVESVPGYPRRLHASWTYPASWRRQPHFLL--KFRLQYRPAQ
                                                                                                                                                                                                                       VLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALK---DFLFQAKYQIRYRVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: WIDELY EXPRESSED.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: PART OF THE RECEPTOR FUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ONTAINS ONE
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                        -----WGTPSTGPLQDEIPD---WSQGH
                                                                                                                                                                                                                                                                                                                                                                                               10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              46655 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE RECEPTOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TO THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                 . 43;
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                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA AND A BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         F65B3060 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             204; DB 11;
No. 4.7e-11;
422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin fold; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERLEUKIN
BUT DOES NOT
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 432;
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                                                                                                                                                                                                                                                                                                                                                                              56;
                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Q16542; Q14626; 01-NOV-1996 (T)

(TrEMBLrel. 01,

Created)

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RAPPERE ROSSON
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                01-FEB-1997 (TIEMBLIEL 02, Created)
01-FEB-1997 (TIEMBLIEL 02, Last sequence update)
01-NOV-1998 (TIEMBLIEL 08, Last annotation update)
INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2 PRECURSOR (IL
(IL-11RBETA) (INTERLEUKIN-11 RECEPTOR BETA CHAIN).
IL11RA2 OR IL-11RBETA.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
INTERLEUKIN-11 RECEPTOR.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MINVIELLE S., JACQUES Y.; "Molecular cloning of two hematopoletic cytokine int Blood 86:2534-2540(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAN LEUVEN F., STAS 1
Submitted (SEP-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 3-390 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-PLACENTA;
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                                                                                                             0225; 009074;
                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                      VCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYK 98
                                                                                                                                                                                                                          HPAWSTVEP
                                                                                                                                                                              EA---
                                                                                                                                                                                                  TAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLGWLKKH
                                                                                                                                                                                                                                             SVDWKVVDDVSNQTSCRLAGLK------PGTVTFVQVRCNPFGIYGSKKAGIWSEWSHP 257
                                                                                                                                                                                                                                                                  LLDVSLQSILRPDPPQGLRVESVPGYPRRLRASWTYPASWPCQPHFLL--KFRLQYRPAQ
                                                                                                                                                                                                                                                                                        VLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSP---PALKDFLFQAKYQIRYRVED
                                                                                                                                                                                                                                                                                                              KKTVLGADSQRRSPSTGPWPC--PQDPLGAARCVVHGAEFWSQYRINVTEVNPLG-ASTR
                                                                                                                                                                                                                                                                                                                                 LRWYGQDNTCEEYHTVGPHSCHIPKD------LALFTPYEIWYEATNRIGSARSD 147
                                                                                                                                                                                                                                                                                                                                                        ICQTLDGALGGTVTLQLGYPPARPV-VSCQAADYENFSCTWSPSQ--ISGLPTRYLTSYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z46595:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U32324; AAB36492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAA86570.1;
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۲:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           45222 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                              10.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEBEAU B.,
                                                                                                                                                                                                                       -- AGLEEVITDAVAGLPHAVRVSARDF----LDAGTWSTWS-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin-11.";
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100,
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                                                                                                                                                                            WGTPSTGTIPKEIP---AWGQLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                               Score 203;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata;
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           29011292 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIORNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEBEAU
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                                                                                                                        432
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                                                                                                                                                                                                                                                                                                                                                                                                     106;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 422;
                                                                 (IL11RA2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α.,
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                                                                                                                                                                                                                                        Query Match
Best Local s
Matches 65
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EMBL; X94158; CAA63872
EMBL; X94159; CAA63872
EMBL; X94160; CAA63872
EMBL; X94161; CAA63872
EMBL; X94161; CAA63872
                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of a second murine interleukin-11 receptor alpha-chain gene (ILIIRa2) with a restricted pattern of exp Genomics 40:387-394(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
STRAIN-CD1; TI
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROBB L., HILTON D.J., WILLSON T.A., BEGLEY C.G "Structural analysis of the gene encoding the receptor alpha-chain and a related locus."; Biol. Chem. 271:13754-13761(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Two differentially expressed interleukin-11 nouse genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                   FRANSMEM
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                                                                             148
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
TISSUE SPECIFICITY: WIDELY EXPRESSED.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONTAINS ONE IG-LIKE DOMAIN
SVDWKVVDDVSNO--TSCRLAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSEWSHPTAAST
                                                                            VLTLDILDVVTTDPPPDVHVSRVGGLEDQLSVRWVSPPALK - - - DFLFQAKYQIRYRVED
                                                                                                                                           LRWYGQDNTCEEYHTVGPHSCHIPKD-----LALFTPYEIWVEATNRLGSARSD 147
                                                                                                                                                                          VCQTLDGVSGGMVTLKLGFPPARP-EVSCQAVDYENFSCTWSPGQ--VSGLPTRYLTSYR
                                                                                                                                                                                                        VCHARDGSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYK
                                              LLDVRLQSILRPDPPQGLRVESVPGYPRRLHASWTYPASWRRQPHFLL--KFRLQYRPAQ
                                                                                                             KKTLPGAESQRESPSTGPWPC--PQDPLEASRCVVHGAEFWSEYRINVTEVNSLG-ASTC
                                                                                                                                                                                                                                                        Similarity
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97129000.
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                                                                                                                                                                                                                                                                                                                       46721
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1; JOINED.
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Pred.
                                                                                                                                                                                                                                                                                                                                      v ;
                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL) IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERLEUKIN-11 RECEPTOR ALPHA CHAIN EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                      -> P (IN CAA63872).
-> L (IN CAA63872).
C4FD7DEC CRC32;
                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                       195;
No. 3.
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                                                                                                                                                                                                                                                       DB 1
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                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fold; Signal.
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                                                                                                                                                                                                                                        34;
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Best Local Similarity 27.6
Matches 75; Conservative
311 ---SSKLHLSGGSWSNWSESLRTRTPEEEPVG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1270861; IL12RB2.
PFAM; PF00041; fn3; 4.
SEQUENCE 874 AA; 98196
                                        241 GIYGSK----KAGIWSEWSHPTAASTPRSERPG 269
                                                                               262 W-----EDEGQYVLNQLRYQPLNSTSWNMVNATNAKGKYDLRDLRPFTEYEFQI-----
                                                                                                                          181 WVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQVRCNPF 240
                                                                                                                                                                     203 LSPDLA-ESRFIVRVTAINDLGNSSSLPHTFTFLDIVIPLPPWDIRINFLNASGSRGTLQ 261
                                                                                                                                                                                                 121 IPKDLALFTPYEIWVEATNRLGSARSDYLTLDILDVYTTDPPPDYHVSRYGGLEDQLSVR 180
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RESKY D.H., YANG H., MINETTI L.J., CHUA A.O., NABAVI N., WOU C.Y., SATELY M.K., GUBLER U.;

Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.

BMBL; U64199; AAB36676.1;
                                                                                                                                                                                                                                                          149 GENGTVACSWNSGK--VTYLKTNYTLQLS----GPNNLTCQKQCFSDNRQNCNRLDLGIN 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lus musculus (Mouse).
Jukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Jutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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11-MAY-1997 (TrEMBLrel. 03, Last sequence update)
11-NOV-1998 (TrEMBLrel. 08, Last annotation update)
11-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                       98 QVTNLSLGMTLFVCKLNCSNSQKKPPVPVC-----GVEISVGVAPEPPQNISCVQE 148
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98196 MW;
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Search completed: September 16, 1999, 20:40:09 Job time: 5560 sec

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1006
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υπ · co	A 24 95 8	RLLNTSTLALANLN : : : : TIINRTASSVTFTDIA	OY 2 PTLLIGSSLQATCSIHGDTPGATAEGLYWTFNGRRLPSELSRLLNTSTLALALANLN
ω	Gaps	Length 708; Indels 5;	Query Match 13.3%; Score 133.5; DB 1; Best Local Similarity 27.3%; Pred. No. 8.4e-07; Matches 35; Conservative 22; Mismatches 66;
			PE:
			CHARACTERIST 708 amino AMINO ACID Y: linear
	•		TELEPHONE: 206-587-0430 TELEPHONE: 206-587-0606 INFORMATION FOR SEO ID NO: 2:
		· .	Seese, Ka RATION NUM NCE/DOCKET
			; APPLICATION NUMBER: US/07/797,556 FILING DATE: 19911122 ; CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION:
			: Floppy disk IBM PC compatib YSTEM: PC-DOS/ PatentIn Releas CATION DATA:
			STATE: WA COUNTRY: USA IP: 98101 COMPUTER READABLE FORM:
			BER OF SEQUENCES: 17 RESPONDENCE ADDRESS: DDRESSEE: Immunex Corporatio TREET: 51 University Street ITY: Seattle
		od Leukemia	PATENT OF SECTION OF STATE OF
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RESULT 2 US-08-308-881-2

Sequence 2, Application US/08308881 Patent No. 5783672

ENERAL INFORMATION

Receptor for Oncostatin

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Query Match
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COUNTRY: U
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PPLICATION NUMBER: US 08/249,553
ILING DATE: 26-MAY-1994
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                                                                                MEDIUM TYPE: Floppy
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LING DATE: 26-MA
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CATION NUMBER: PCT/US95/06530
                 RE: PatentIn Release #1.0, Version #1.25 APPLICATION DATA:
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Receptor for Oncostatin M and Leukemia
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Pred. No. 8.
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EFERENCE/DOCKET NUMBER: EGISTRATION NUMBER

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Kathryn A

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Matches
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CURRENT APPLICATION DATA:
US/07/943,843
                                                       EQUENCE CHARACTERISTICS:
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                                                                                                                             NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 26
                                                                                                                                                                                                       APPLICATION NUMBER: US
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VENTION: Leukemia Inhibitory Factor Receptors
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Pred. No. 0.00016;
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----AHGETFLHTNYSLKYKLRLVRSE 135

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US-07-943-843-6
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US-07-943-843-6
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SEQUENCE CHARACTERISTICS:
LENGTH: 1097 amino aci
TYPE: AMINO ACID
                                                                                                                                                                                                                                             MOLECULE TYPE:
298 AIKIRNISVS-ASSGINVVFTTEDN--IFGTVIFAGYPPDTPQQLNCETHDLKEIICSWN 354
                                                                  258 DKVILVGSDITFCCVSQEKVLSALIGHTNCPLIHLDG---
                               51 ALALANINGSROOSGDNIVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 PGRVTALVGPRATSYTLVE-SFSGKY-VRLKRAE 386
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                                                                                                1 DPTLLIGSSLQATCSI------HGDTPGATAEGLYWTFNGRRLPSELSRLLNTSTL 50
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                                                                                                                                                                                                                                                                                                                                                                                                       LASSIFICATION:
LASSIFICATION:
IORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
NAME: Seese, Kathryn A.
NAME: 32,172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLING DATE: 19920911
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                                                                                                                                                                                                                                                                                                                                                                                                EFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OFTWARE: Patentin Rela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OMPUTER: IBM PC compatible PERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No.
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PGRVTALVGPRATSYTLVE-SFSGKY-VRLKRAE 386

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Best Local
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                                                                                                                                                                                                                                               51 ALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWT 110
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57
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                                Gearing, David P.
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eukemia Inhibitory Factor Receptors
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                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                            111 PG-----AHGETFLHTNYSLKYKLRLVRSE 135
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ORNEY/AGENT INFORMATION:
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                                                                                                     UNTRY:
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                                                                                                                                        Seattle
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DATE: 11-SEP-1992
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                                                                                                                                                          51 University Street
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51 University Street
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PC-DOS/MS-DOS
Release #1.0,
                                                                                                                                                                            Corporation
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Pred. No. 0.00018;
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 Version #1.25
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                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                              TELEPHONE: 206-587-0430
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                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
          JUENCE CHARACTERISTICS:
JENGTH: 719 Pmin
                                                                                                                                                         APPLICATION NUMBER: US 0
FILING DATE: 11-SEP-1992
FORNEY/AGENT INFORMATION:
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29; Conservative
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amino acid
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51 University Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leukemia Inhibitory Factor Receptors
                                                                                                                                                                                           US 07/943,843
                                                                                                                                                                                                                                                           US/08/347,003
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                                                                                                              2606-в
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 112.5; DB 1; Pred. No. 0.00019;
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Best Local S1
Matches 29;
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                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (201) 235-23
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
141 VACTWERGR--DIHLYTEYTLQ--
                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE CHARACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         URRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 DKVVLAGSNWTICCM----SPTKVLSG-----QIGNTLRPLIHLYGQTVAIHILNIP 300
                                 105 LTCRWTPGAHGETFLHTNYSLKYKLRLVRSEXHMXGVPHCEPSLMPY--
                                                                       95
                                                                                                                                                                                                                            Match 11.0%;
Local Similarity 21.5%;
                                                                                                     46 NTSTLALALANINGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMK-D 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 GSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPG 112
                                                                                                                                        41 ILLGSTVNITCSL-----KPRQGCFHYSRRNKLILYKFDRRINFHHGHSLNSQVTGLPL 94
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                         4 LLIGSSLOATCSINGDTPGATAEGLY------WTF-----NGRRLPSELSRL-L 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLICATION NUMBER:
                                                                       GTTLFVCKLACINSDEIQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.28;
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                                                                                                                                                                                                                                Score 110.5;
Pred. No. 0.
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Pred. No. 0.00019;
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-LSGPKNLTWQKQCKDIYCDYLDFGINLTPESPE 193
                                                                                                                                                                                                              Mismatches
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                                                                  ---ICGAEIFVGVAPEQPQNLSCIQKGEQGT 140
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                                                                                                                                                                                                                                           Length 862;
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                                 ----PQGP- 156
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156 ----GPLHSLXDLGGSHQSP 171

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Best Local Similarity
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                        156 ----GPLHSLXDLGGSHQSP 171
                                                     141 VACTWERGR--DTHLYTEYTLQ-----LSGPKNLTWQKQCKDIYCDYLDFGINLTPESPE 193
                                                                                  105 LTCRWTPGAHGETFLHTNYSLKYKLRLVRSEXHMXGVPHCEPSLMPY------PQGP- 156
194 SNFTAKVTAVNSLGSSSSLP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTORNEY/AGENT INFORMATION
                                                                                                                                              46 NTSTLALALANINGSROQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMK-D 104
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                                                                                                               95 GTTLFVCKLACINSDEIQ-------ICGAEIFVGVAPEQPQNLSCIQKGEQGT 140
                                                                                                                                                                             41 ILLGSTVNITCSL-----KPRQGCFHYSRRNKLILYKFDRRINFHHGHSLNSQVTGLPL 94
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                          4 LLIGSSLOATCSIHGDTPGATAEGLY------WTF-----NGRRLPSELSRL-L 45
                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
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E OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                         TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                     862 amino acids
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                                                                                                                                                                                                                                                          11.0%;
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                                                                                                                                                                                                                                                             Score 110.5;
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Query Match
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                                                                149 -ETHLPTSFTLKSFKSRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLY-QNMGIWVQAE 206
207 NALGTSMSPQL 217
                                  163 DLGGSHQSPRL 173
                                                                                                      115 GETFLHTNYSLK-YKLR---LVRSEXHMXGVP-----HC---EPSLMPYPQGPGPLHSLX 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELECOMMUNICATION INFORMATION:
                                                                                                                                                                           59 GSRQQSGDNLVCHARDGS---ILAGSCLYVGLPPEKPFNISC-WSRNMKDLTCRWTPGAH 114
                                                                                                                                                                                                               34 PIVHLGDPITASCIIKQNCSHLDPEPQILWRLGAELQPGGRQQRLSDGTQESIITLPHLN 93
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                  2 PTILIGSSIQATCSIHGDTPGATAE-GLYWTFNGRRLPSELSRLLN--TSTLALALANLN 58
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                                                                                                                                       HTQA----FLSCCLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLICQWEPGP-
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G DATE: 03-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                           : 836 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: protein
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                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones, Tullar & Cooper, P.C.
). Box 2266 Eads Station
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03-JUL-1990
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Pred. No. 0.0061;
                                                                                                                                                                                                                                                                                                                              DB 1;
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RESULT 14 US-07-923-976-6

Sequence 6, Application US/07923976 Patent No. 5574136

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Query Match
Best Local Similarity
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                                                                         -923-976-8
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 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 74539/1990
                                                                                                                                             207 NALGTSMSPQL 217
                                                                                                                                                                                                            149 -ETHLPTSFTLKSFKSRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLY-QNMGIWYQAE 206
                                                                                                                                                                                                                                                115 GETFLHTNYSLK-YKLR---LVRSEXHMXGVP-----HC---EPSLMPYPQGPGPLHSLX 162
                                                                                                                                                                              163 DLGGSHQSPRL 173
                                                                                                                                                                                                                                                                                                                      59 GSRQQSGDNLVCHARDGS---ILAGSCLYVGLPPEKPFNISC-WSRNMKDLTCRWTPGAH 114
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                                                                                                                                                                                                                                                                                           94 HTQA----FLSCCLNWGNSI
                                                                                                                                                                                                                                                                                                                                                          34 PIVHLGDPITASCIIKQNCSHLDPEPQILWRLGAELQPGGRQQRLSDGTQESIITLPHLN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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ELEPHONE: 703-415-1500
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                                                                                                                                                                                                                                                                                                                                                                                            PTILIGSSLQATCSIHGDTPGATAE-GLYWTFNGRRLPSELSRLLN--TSTLALALANIN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATE: 03-JUL-
PLICATION DATA:
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TYPE: Floppy disk
TYPE: Floppy disk
ER: IBM PC compatible
ER: IBM PC-DOS/MS-DOS
                                                    Application US/07923976
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Nagata, Shigekazu
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03-JUL-1990
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22-MAR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.9%; Score 100; DB 1; 26.7%; Pred. No. 0.0054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Encoding Granulocyte
Colony-Stimulating Factor Receptor
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                                                                                                                                                                                                                                                                                      COILDQVELRAGYPPAIPHNLSCLMNLTTSSLICQWEPGP- 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 771
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                   163 DLGGSHQSPRL 173
                                                                  149 -ETHLPTSFTLKSFKSRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLY-QNMGIWVQAE 206
                                                                                                      115 GETFLHTNYSLK-YKLR---LVRSEXHMXGVP----HC---EPSLMPYPQGPGPLHSLX 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACT
207 NALGTSMSPQL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                         94 HTQA----FLSCCLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLICQWEDGP- 149
                                                                                                                                                                          59 GSRQQSGDNLVCHARDGS---ILAGSCLYVGLPPEKPFNISC-WSRNMKDLTCRWTPGAH 114
                                                                                                                                                                                                             34 PIVHLGDPITASCIIRQNCSHLDPEPQILWRLGAELQPGGRQQRLSDGTQESIITLPHLN 93
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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STATE: Virginia
ZIP: 22202
                                                                                                                                                                                                                                                 2 PTILIGSSLQATCSIHGDTPGATAE-GLYWTFNGRRLPSELSRLLN--TSTLALALANLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 03-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ON NUMBER:
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Box 2266 Eads Station
                                                                                                                                                                                                                                                                                                                                                                                                         protein
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03-JUL-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Encoding Granulocyte Colony-Stimulating Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT/JP91/00375
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                                                                                                                                                                                                                                                                                                          Score 100; DB 1;
Pred. No. 0.0063;
                                                                                                                                                                                                                                                                                                                             Length 863;
                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                     Gaps
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11;

completed: September 16, 1999, 20:41:11 he: 5440 sec

R70125 R86868

LIF-R-GBP 130 fusi IgG1 Fc region and

ALIGNMENTS

cancer;

OM protein protein search, using sw model

9 September 17, 1999, 03:08:16; Search time 64.1 Seconds (without alignments) 68.730 Million cell updates/sec

Scoring table: Perfect score: BLOSUM62 DPTLLIGSSLQATCSIHGDT..

.....SHQSPRLSKIXCPHTGCPGR 186

US-09-037-657-29

Searched: 188963 seqs, 23686106 residues

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

409	08765A	26 28 28 29 13 30 13 31 13 13 13	5 5	1 W 4 10 10 1- 00 0	11109876	143841	esult No. Sc
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Query Match Best Local Matches 184;

Similarity

97.8%;

Score 984; DB 1; Le Pred. No. 1.1e-97;

Length 186;

Indels

0; Gaps

0

Conservative

0

e.g. for cancers or predisposition to cancers,

The products can

ronal proliferation, differentiation be used for detection and diagnosis, o cancers, or for drug screening.

186 AA;

ind survival.

herapeutics used for modulating

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TGCPGR 186

121

121

TNYSLKYKLRLVRSEXHMXGVPHCEPSLMPYPQGPGPLHSLXDLGGSHQSPRLSKIXCPH

TNYSLKYKLRLVRSGXHMXGVPHCGPSLMPYPQGPGPLHSLXDLGGSHQSPRLSKIXCPH

180 180 120 120

RQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH

ROQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH

61

13

1 DPTLLIGSSIQATCSIHGDTPGATAEGLYWTFNGRRLDSELSRLLNTSTLALALANLNGS 60

DPTLLIGSSLQATCSIHGDTPGATAEGLYWTFNGRRLPSELSRLLNTSTLALALANLNGS 60

181 181

TGCPGR 186

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e.g. neuronal cells claim 19; Page 114-115; 182pp; English.

The NR6 protein is a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of the receptors of the result in the receptors of the resent in the receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Stop codon"
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Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W55016 standard; Protein; 186 AA.
W55016;
                                                                                                                                                                                                                         ew isolated haemopoietin receptor - used for developing products or modulating proliferation, differentiation and survival of cells,
                                                                                                                                                                                                                                                                                         7-PSDB; V27145
                                                                                                                                                                                                                                                                                                                                                A-SEP-1996; AU-002246.
AMRAD OPERATIONS PTY LTD.
DZIEGLEWSKA H E.
LEXANDER W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Cojima T, Maeda M, Nash A, Nicola NA, Rakar S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of Murine NR6
                                                                                                                                                                                                      or modulating proliferation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-1998
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1-SEP-1997; G02479.
                                                                                                                                                                                                                                                                                                           98-260970/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Stop codon"
139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferation; drug screening;
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                                          WO9811225-A2.
19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The haemopoletin receptor (HR) NR6.1 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis,
                                                                                                                                                                                                                                                                                       Novel haemopoietin 
Haemopoietin recept
                                                                                                                                                                                                                                                               cell survival;
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(DZIE/) DZIEGLEWSKA H E.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, Hilton DJ, Kikuchi Y,
Alexander W, Fabri L, Parley A, Hilton DJ, Kikuchi Y,
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§55012 standard;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
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    modulating prol
    neuronal cells

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPTLLIGSSLQATCSIHGDTPGATAEGLYWTFNGRRLPSELSRLLNTSTLALALANLNGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETELH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134;
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receptor; cell
l; therapeutic;
  Fabri L, Farl
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                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or predisposition to cancers,
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tor; cell
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                                                                                                                                                                                                                                                                                                                                       entry)
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Farley A, Hilton
sh A, Nicola NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182pp;
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                                                                                                                                                                                                                                                         r NR6.2 protein.
l proliferation;
neuronal prolif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NR6.1 protein. proliferation; cell difineuronal proliferation;
                                                                                                                                                                                                                                                                                                               NR6.2
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Pred. No. 9.7e-67;
0; Mismatches 8
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                        Hilton
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     Rakar
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                                                                                                                                                                                                                                                                                    cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        developing products and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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Willson
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Best Local Sim
Matches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and survival.
e.g. for cancer
Sequence 425
                                                  haematopoietin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant up protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases,
cancer, and allergy).
Sequence 425 AA;
                                                                                                                                                                                                                                                                                                               New nucleic acid encoding U4 haematopoietin re chain - potentially useful, e.g. for modulatin or immune response, for treating cancer and au claim 9; Pages 26-27; 38pp; English.

This is the amino acid sequence of the murine beautiful and sequence of the murine beautiful and sequence of the murine beautiful acid sequence of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence
Murine; U4 protein;
cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to regulate development, maintenance or regeneration in an array of different cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and survival. The products can also be used for detection and diagnosis, e.g. for cancers or predisposition to cancers, or for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 98-414109/35.
N-PSDB; V41688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUL-1998.
15-JAN-1998; U00334.
16-JAN-1997; US-784863
(GEMY) GENETICS INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated haemopoietin rector modulating proliferation, e.g. neuronal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collins M, Donaldson DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The haemopoietin receptor (HR) NR6.2 is a form of the novel HR NR6. Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang J;
WPI; 98-260970/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W59804 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; Page 84-87; 182pp;
The haemopoietin receptor (H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNYSLKYKLRWYGQDNTCEEYHTVG-PH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
of the murine U4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune response; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.5%;
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1, e.g. for modulating cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 699; DB 1 Pred. No. 1e-66; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
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                                                                                                                                                                                                                                                                                                                                                                         modulating cell procer and auto:immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  developing products and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell differentiation;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-log ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T,
Adams RL, Foster DE, Whitmore TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Zcytor5 variant.

Zcytor5; cytokinin-like receptor; down-regulation; growth factor; Zcytor5; cytokinin-like receptor; skeletal muscle; cardiotrophin-l; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a Zcytor5 variant is a cytokinin-like receptor. Soluble Zcytor5 may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W70841 standard;
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   130
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                                                                                                                                                                                                                                                                                                             1 DPTLLIGSSLOATCSIHGDTPGATAEGLYWTFNGRRLPSELSRLLNTSTLALALANLNGS
TNYSLKYKLRWYGQDNTCEEYHTVG-PH
                                                                 TNYSLKYKLRL-----VRSEXHMXGVPH 143
                                                                                                                                                                   RQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWIPGAHGETFLH 120
                                                                                                                                                                                                                                                                     DPTLLIGSSLHATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGS
                                                                                                                               RQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 694; DB 1
Pred. No. 3e-66;
D; Mismatches
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0; Mismatches
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156
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and anti-idiotypic antibody could be used to purify Zcytor5 and therapeutically to modify Zcytor5 ligand effects.
                                                                                                                                   02-0CT-1998 (first entry)
Protein sequence of products generated by 5N race of brain cDNA.
Haemopoietin receptor; cell proliferation; cell differentiation; cell survival; therapeutic; neuronal proliferation; drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a protein designated Zcytor5, which a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect
(AMRA-) AMRAD OPERATIONS PTY LTD.
(DZIE/) DZIEGLEWSKA H E.
Alexander W, Fabri L, Farley A, F
                                                  19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-0022
                                                                                                                                 Mouse
                                                                                                                                                                                                                         W55014 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 75-76; 55pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mammalian cytokinin-like receptor Zcytor5
down-regulating Zcytor5 natural ligands or de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; V70896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (2YMO) ZYMOGENETICS INC. Adams RL, Foster DC, Gilt Lok S, Presnell SR, Whitn WPI; 99-034662/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiac pathology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             maintenance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zcytor5; cytokinin-like receptor; down-regulation;
maintenance factor; thyroid; heart; skeletal muscl
cardiac pathology; heart enlargement; zcytor5 liga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W70862 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                      110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9849307-A1.
                                                                                                                                                                                                                                                                                                        170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                )1-MAY-1997;
                                                                                                                                                                                                                                                                                                                                    121 TNYSLKYKLRL----VRSEXHMXGVPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .7-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DPTLLIGSSLQATCSIHGDTPGATAEGLYWTFNGRRLDSELSRLLNTSTLALALANLNGS
                                                                                                                                                                                                                                                                                                                                                                                    RQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH
                                                                                                                                                                                                                                                                                                                                                                                                                              DPTLLIGSSLHATCSIHGDTPGATAEGLYWTLNGRRLPSELSRLLNTSTLALALANLNGS
                                                                                                                                                                                                                                                                                                     TNYSLKYKLRWYGQDNTCEEYHTVG-PH
                                                                                                                                                                                                                                                                                                                                                                  RQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-074721
US-045287
                                                  AU-002246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whitmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.0%; Score 694; DB 1; I
89.9%; Pred. No. 3.5e-66;
Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425
                                                                                                                                                                                                                         278 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
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    Hilton DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jelmberg AC,
                                                                                                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                                                     196
    K1kuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or5 - useful for, e.g.
detecting cardiotrophin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ation; growth
muscle; cardi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lehner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
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                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                              109
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rade a service service
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Best Local
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                haematopoletin receptor superfamily, used in the method of the invention for the modulation of cell proliferation, or the immune response. Transformed mammalian cells are used to produce recombinant U4 protein. The U4 protein is used to screen for specific binding agents, raise antibodies. It is also used as reagents for assays and as tissue markers for isolation of cognate ligands and receptors, and in pharmaceutical compositions which may modulate cell proliferation, cell differentiation, and the immune system (e.g. for treating immune deficiency, inherited or the result of infection, autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding U4 haematopoletin receptor superfamily chain - potentially useful, e.g. for modulating cell proliferation or immune response, for treating cancer and auto:immune disease claim 9; Pagees 29-30; algop; English.

This is the amino acid sequence of the human U4 protein from the haematopoletin receptor superfamily, used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEMY) GENETICS INST INC
Collins M, Donaldson DD,
WPI; 98-414109/35.
N-PSDB; V41689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The protein sequence was generated by a 5N RACE of brain cDNA using NR6 specific primers: NR6 is a novel Haemopoletin receptor (HR). Interaction between the novel HR and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The HR and it's derivatives can be used for modulating the activity of the receptors e.g. to regulate development, maintenance or regeneration in an array of differentiation cells and tissues in vitro and in vivo. They can be present in therapeutics used for modulating neuronal proliferation, differentiation and diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; U4 protein; haematopoietin receptor cell proliferation; immune response; antibo autoimmune disease; cancer; allergy.
cancer, and allergy).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
WO9831811-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g. for cancers or predisposition to cancers, Sequence 278 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W59805 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for modulating proliferation, e.g. neuronal cells Claim 17; Page 93-95; 182pp; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6-JAN-1997; US-784863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolated haemopoietin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYSLKYKLRL----VRSEXHMXGVPH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYSLKYKLRWYGQDNTCEEYHTVG-PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98-260970/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nash A, Nicola NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune response; antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neben T, Whitters M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor - used for ion, differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Pred. No. 2.5e-66;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₹
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   superfamily;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developing products and survival of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or for drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Willson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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130

TNYSLKYKLRWYGQDNTCEEYHTVG-PH

156

TNYSLKYKLRL----

-VRSEXHMXGVPH 143

70 61 Query Match Best Local

Similarity

65.4%;

Score 658; DB Pred. No. 2.2e 4; Mismatches

DB 1; .2e-62;

Length

13;

Indels

6

Gaps

Ņ

Conservative

Matches

10

1 DPTLLIGSSIQATCSIHGDTPGATAEGLYWTFNGRRLDSELSRLLNTSTLALALANLNGS

RQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH 120 DPTILIGSSLLATCSVHGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGS

RQRSGDNLVCHARDGSILAGSCLYYGLPPEKPYNISCWSKNMKDLTCRWTPGAHGETFLH

129

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Best Local S
Matches 125
        The present sequence represents a Zcytor5 variant protein. Zcytor5 is a cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-l in the blood, and to discover other possible Zcytor5 igands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1998;
01-MAY-1998;
13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l;
cardiac pathology; heart enlargement; Zcytor5 ligand; variant.
                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                         down-regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lok S, Presnell SR, Whitmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams RL, Foster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1997; US-04
01-MAY-1997; US-85
                                                                                                                                                                                                                                                                                                                                                                                                                New mammalian cytokinin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Zcytor5
                                                                                                                                                                                                                                                                                                                                                               in blood
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125; Conser
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natural ligands or detecting cardiotrophin-1
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No. 2.3e-62;
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Best Local :
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                                Homo sapiens.
WO9849307-A1.
05-NOV-1998.
01-MAY-1998; U08865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a Zcytor5 variant protein. Zcytor5 is a Cytokinin-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to determine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zcytor5 ligand effects.
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                                                                                                Zcytor5; cytokinin-like receptor; down-regulation;
maintenance factor; thyroid; heart; skeletal muscl
                                                                                                             Human Zcytor5 variant
Zcytor5; cytokinin-11
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WPI; 9
        13-FEB-1998; US-074721
01-MAY-1997; US-045287
                                                                                       cardiac
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Adams RL, Foster
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maintenance factor; thyroid; heart; skeletal muscle
cardiac pathology; heart enlargement; 2cytor5 ligar
                                                                                                                                                                W70850 standard; Protein; 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             down-regulating
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01-MAY-1997; US-045287
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                                                                                                                                                                                                                                                                                               RQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH
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125; Conser
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                                                                                    pathology; heart enlargement;
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                                                                                                                                     (first entry)
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.2e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 389;
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                                                                                              cardiotrophin-1;
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Best Local
                                        The present sequence represents a Zcytor5 variant protein. Zcytor5 is a cytokini-like receptor. Soluble Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-l on cardiac pathologies, so preventing heart
 blood, and to discover other possible Zcytor5 ligands. comprising Zcytor5 DNA or RNA can be used to determine
                          of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the
                                                                                                                                                                                                (ZYMO) ZYMOGENETICS INC.
Adams RL; Foster DC, Gilbert
Lok S; Presell SR, Whitmore
                                                                                                                          Claim 1; Page 96-97; 55pp;
                                                                                                                                            in blood
                                                                                                                                                       New mammalian cytokinin-like receptor 20 down-regulating Zcytor5 natural ligands
                                                                                                                                                                                        WPI; 99-034662/03
                                                                                                                                                                                                                                                                      01-MAY-1997;
01-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                cardiac pathology;
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W70851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New mammalian cytokinin-like receptor Zcytor5 down-regulating Zcytor5 natural ligands or det
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Adams RL, Foster DC,
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US-045287
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, Gilbert T, Jr
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                                                                                                                          English
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Pred. No. 2.2e-62;
4; Mismatches 13;
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to determine the
                                                                                                                                                     detecting cardiotrophin-1
                                                                                                                                                                                                                   Lehner
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    useful for,

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cting cardiotrophin-l
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                probe
presence
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Best Local
                                                                                                                                                    down-regulate the effects of a growth and/or maintenance factor in thyroid, heart, and skeletal muscle for example to lessen the effect of cardiotrophin-1 on cardiac pathologies, so preventing heart enlargement. Zeytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zeytor5 ligands. A probe comprising Zeytor5 NA or RNA can be used to determine the presence and integrity of the Zeytor5 gene on chromosome 19. Antibodies and therapeutically to modify Zeytor5 ligand effects.
                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert T,
Lok S, Presnell SR, Whitmore TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and integrity of the Zcytor5 gene on chromosome 19. Ant: anti-idiotypic antibody could be used to purify Zcytor5 therapeutically to modify Zcytor5 ligand effects.
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                                                                                                                                                                                                                                                                                             The present
                                                                                                                                                                                                                                                                                                                                down-regulating Zcytor5 natural ligands
                                                                                                                                                                                                                                                                                                                                            New mammalian cytokinin-like receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiac pathology; heart enlargement;
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                                             present sequence represents a Zcyt cytokinin-like receptor. Soluble
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RORSGDNLVCHARDGSILAGSCLYYGLPPEKPYNISCWSKNMKDLTCRWTPGAHGETFLH
             ROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH
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125; Conserv
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                                                                                                             Similarity
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nce factor; thyroid; heart;
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Pred. No. 2.2e
4; Mismatches
                                                                                                          Score 658; DB 1;
Pred. No. 2.2e-62;
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t; skeletal_muscl
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    useful for, e.g.
    tecting cardiotrophin-1

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e; cardiotrophin-1;
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In blood

Claim 1; Page 99-100; 55pp; English.

Claim 1; Page 99-100; 55pp; English.

Che present sequence represents a Zcytor5 wariant protein. Zcytor5

Claim 2; Page 99-100; 55pp; English.

Chyrolidin present sequence represents a Zcytor5 may be administered to down-regulate the effects of a growth and/or maintenance factor in the control of cardiotrophin-1 on cardiac pathologies, so preventing heart confirmed protects could be used to detect cardiotrophin-1 in the enlargement. Zcytor5 could be used to detect cardiotrophin-1 in the blood, and to discover other possible Zcytor5 ligands. A probe comprising Zcytor5 DNA or RNA can be used to deternine the presence and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the thorse anti-idiotypic antibody could be used to purify Zcytor5 and the the presence anti-idiotypic antibody could be used to purify Zcytor5 and the the presence anti-idiotypic antibody could be used to purify Zcytor5 and the the presence anti-idiotypic antibody could be used to purify Zcytor5 and the the presence anti-idiotypic antibody zcytor5 ligand effects.
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  Query Match
Best Local (
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01-MAY-1998; U08865.
13-FEB-1998; US-074721.
01-MAY-1997; US-045287.
01-MAY-1997; US-850030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Zcytor5 variant.
Human Zcytor5; cytokinin-like receptor; down-regulation; growth factor; Zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l; cardiac pathology; heart enlargement; Zcytor5 ligand; variant.
                                                                                                                                                                                                                                                                                                                                                                                                            Lok s,
                                                                                                                                                                                                                                                                                                                                                    down-regulating
                                                                                                                                                                                                                                                                                                                                                                          New mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO) ZYMOGENETICS INC.
Adams RL, Foster DC, Gilbert
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Presnell SR, Whitmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein;
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US-023890
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ng Zcytor5 natural ligands or detec
  65.48;
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cardiotrophin-1
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Matches
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                TNYSLKYKLRL----VRSEXHMXGVPH 143
                                                                       RQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH
                                                                                                                              DPTLLIGSSLQATCSIHGDTPGATAEGLYWTFNGRRLPSELSRLLNTSTLALALANLNGS
TNYSLKYKLRWYGODNTCEEYHTVG-PH
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RESULT 15
W70840
ID W70840 standard; Protein; 392 AA.
AC W70840;
DT 17-MAR-1999 (first entry)
DE Human Zcytor5 variant.
KW Zcytor5; cytokinin-like receptor;
KW Zcytor5; cytokinin-like receptor;
KW maintenance factor; thyroid; hear
KW cardiac pathology; heart enlargem
OS Homo saplens.
PN W09849307-A1.

Human Zcytor5 variant.

Zcytor5; cytokinin-like receptor; down-regulation; growth factor; maintenance factor; thyroid; heart; skeletal muscle; cardiotrophin-l; cardiac pathology; heart enlargement; Zcytor5 ligand; variant.

Homo sapiens.

W09849307-A1.

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PF 01-MAY-1998; U08865.

PR 13-FEB-1998; US-045287.

PR 01-MAY-1997; US-045287.

PR 01-MAY-1997; US-045287.

PR 01-MAY-1997; US-045287.

PR 01-MAY-1997; US-0452890.

PR 13-FEB-1998; US-023890.

PR 13-FEB-1997; US-02890.

PR 13-FEB-1998; US-02890.

PR 13-FEB-1998; US-02890.

PR 13-F
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Search completed: September 17, 1999, 03:08:16 Job time: 307 sec

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd
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OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:10; Search time 49.27 Seconds (without alignments) 151.252 Million cell updates/sec

US-09-037-657-29 1006

Title: Perfect score:

Sequence: 1 DPTLLIGSSLQATCSIHGDT...SHQSPRLSKIXCPHTGCPGR 186

Scoring table: BLOSUM62

Searched: 122810 seqs, 40065486 residues

Database : PIR_60:* p1r2:* p1r3:* p1r4:* pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

A; Gene: gp130 C; Keywords: glycoprotein

A; Residues: 1-917 < RES>

Molecule type: mRNA

esidues: 1-917 <RE2> ross-references: EMBL:X62646; NID:g840816; PID:g840817

Cross-references: GB:M83336; NID:g193591; PID:g193592 Accession: I48370

translated from GB/EMBL/DDBJ

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٠	ENTS	ALIGNMENTS	•				• • •	
prolactin receptor	prolact	I51086	N	630	7.9	79	45	
leptin receptor, O	leptin	JC4897	ω ,	508	7.9	79.5	44	
leptin receptor pr	leptin	JC4797	, N	894	7.9	79.5	. 4	
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אווללה-ה הסכם	\$ ntorio	A41242		468	æ 0	80	40	

γ 밁 뭥 В Query Match 14.3%; Score 144; DB 2; Length 917; Best Local Similarity 26.5%; Pred. No. 3e-06; Matches 39; Conservative 26; Mismatches 70; Indels 154 LETNYTLK-----SEWATEKFPDCQ 173 119 LHTNYSLKYKLRLVRSEXHMXGVPHCE 145 2 PTILIGSSLQATCSIHG---DTPGATAEGLYWTFNGRRLPSELSRLLNTSTLALALANLN 58 59 GSROQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETF 118 96 LPSYQLTCNILSFGQIEQNYYGYTMLSGFPPDKPTNLTCIVNEGKNMLCQWDPGR--ETY 153 36 PVVQRGSNFTAICVLKEACLQHYYVNASYIVWKTNHAAVPREQVTVINRTTSSVTFTDVV 95 Gaps

ycoprotein gp130 precursor - human

Accession: ., M.; Murakami, 1 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1998 M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.

Title: Molecular cloning and expression of an IL-6 signal transducer, gp130. Reference number: A36337; MUID:91084844 Accession: A36337

Molecule type: mRNA Residues: 1-918 <HIB>

Cross-references: GB:M57230; NID:g186353; PID:g186354

Gene: GDB:IL6ST; GP130

Cross-references: GDB: Map position: 5q11-5q1 glycoprotein; membrane protein GDB:126725; OMIM:600694

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   A; Cross-references:
                                                                          A;Title: Leukemia inhibitory factor receptor is structurally related to the IL-6 signal A;Reference number: S17308; MUID:92007727
                                                                                                                                                                                leukemia inhibitory factor receptor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enomics 14, 666-672, 1992; Title: Molecular cloning a Reference number: A44257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .nterleukin-6 signal transducing molecule
                                               Status: preliminary
                                                                                                     Gearing, D.P.; Thut, C.J.; VandenBos, T.; Gimpel, S.D.; Delaney, P.B.; King,
                                                                                                                                     Accession:
                                                                                                                                                                     Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keywords:
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Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
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Date: 30-Apr-1993
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                              MOLECULE Type:
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                                                                                                                                                                                                                                                                                                                         FQNVQLTCNILSFGQIEQNVYGITILSGYPPDIPTNLSCIVNEGKNMLCQLDPGR--ETY
                                                                                                                                                                                                                                                                                                                                                  GSRQQSGDNLYCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETF 118
                                                                                                                                                                                                                                                                                                                                                                                                             PTLLIGSSLQATCSIHG----DTPGATAEGLYWTFNGRRLPSELSRLINTSTLALALANLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LETNETLK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLNIQLTCNILTFGQLEQNVYGITIISGLPPEKPKNLSCIVNEGKKMRCEWDGGR--ETH 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSROQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETF 118
                                                                                                                                                                                                                                                                                           LHTNYSLKYKLRLVRSEXHMXGVPHC
                                                                                                                                                                                                                                                                                                                                                                                  PVVQRGSNFTATCVLKEKCLQVYSVNATY IVWKTNHVAVPKEQVTVINRTASSVTFTDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVTFTDIA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type: mRN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-918 <WAN>
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                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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 <GEA>: GB:X61615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and characterization of the UDID:93052397
NID: g34365; PID: g34366
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
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Pred. No. 3.
                                                                                                                                                                                                                                                            172
                                                                                                                                                                                                                                                                                           144
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                     10-Nov-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                               130; DB 2;
No. 7.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gp130 -
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                                                                                                                                                   #text_change 20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rat liver
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Query Match

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Length 1097;

GB:D17444; NID:g441493; PID:d1004778;

PID: 9441494

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A:Title: Pregnancy associated A:Reference number: S38942; MT A:Accession: S38942
                                                                                                                          FEBS Lett. 334,
                                                                                                                                                                 A; Experimental
                                                                                                                                                                                                          A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                               differentiation stimulating factor/leukemia inhibitory factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-1092 <TOND
A; Cross-references: DDBJ:D26177; NID:g473718; PID:d1005707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Blochem. 115, 557-562, 1994
A;Title: Three different cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differentiation-stimulating factor/leukemia inhibitory factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Tomida, M.;
                                                                                                                                                                                   Cross-references: DDBJ:D17444; NID:g441493; PID:d1004778;
                                                                                                                                                                                                                                                                                                                                                                      Species: Mus musculus (house mouse)
Date: 28-Aug-1985 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-43/Domain: signal sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Date: 28-Aug-1985 #sequence_revision 07-Oct-1994
                                                                                                                                                                                                                                                                     Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keywords: differentiation; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 DKVVLAGSNMTICCM----SPTKVLSG-----QIGNTLRPLIHLYGQTVAIHILNIP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 PGRVTALVGPRATSYTLVE-SFSGKY-VRLKRAE 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 PG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 AIKIRNISVS-ASSGTNVVFTTEDN--IFGTVIFAGYPPDTPQQLNCETHDLKEIICSWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 DKVILVGSDITFCCVSQEKVLSALIGHTNCPLIHLDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 ALALANLINGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWT | : |: | | | : |: : | : : | : | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 GSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DPTLLIGSSLQATCSIHGDTPGATAEGLYWTFNGRRLPSELSRLLNT--STLALALANLN 58
                                        preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VS-ENSGTNIIFITDDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPTLLIGSSLQATCSI-------HGDTPGATAEGLYWTFNGRRLPSELSRLLNTSTL
                                                                                                                                                                                             type: mkwa
: 1-719 <TOM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                            ; Yamamoto-Yamaguchi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                               Yamamoto-Yamaguchi, Y.; Hozumi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto-Yamaguchi, Y.; Hozumi,
                                                                                                                                                               source: liver
                                                                                                                        193-197, 199:
                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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<TOM2>
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                                                                                                                                                                                                                                                                                      cDNAs encoding mouse D-factor/LIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNAs encoding mouse D-factor/LIF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.2%;
25.4%;
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                                                                             MUID: 94039833
                                                                                                                                            Y.; Hozumi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 112.5; DB 2; Pred. No. 0.0045;
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                                                                                                     soluble
                                                                                                                                                                                                                                                                                                                                                                      #text_change 29-Jan-1999
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                                                                                                 D-factor/LIF receptor
                                                                                                                                                                                   PID: 9441494
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                                                                                                                                                                                                                                                                                                                                                                                                               receptor 2 -
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                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary; translated Molecule type: mRNA Residues: 1~422 <VA2>
                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: cytokine receptor homology CRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /an Leuven, F.
bmitted to the EMBL Data Library, July 1995
Reference number: G08961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ood 86, 2534-2540, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Introns: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL:U32324; NID:g975336; PID:g975337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Dec-1998 Accession: 137891; G01970; G01971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iolecule type: DNA
Residues: 1-422 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reference number:
Accession: G01970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           omitted to the EMBL Data Library, July 1995
Reference number: G08959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic cy
Reference number: 137891; MUID:95399754
Accession: 137891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                terleukin-11 receptor alpha chain -
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                                                                                                             124 SLKYKLRLVRSEXHMXGVPHCEPSLMPYPQGP 155
                                                                      145 LTSYRKKTVLGADSQRRSPSTGP--WPCPQDP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 VS-ENSGTNIIFITDDD--VYGTVVFAGYPPDVPQKLSCETHDLKEIICSWNPG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 DKVVLAGSNMTICCM----SPTKVLSG-----QIGNTLRPLIHLYGQTVAIHILNIP 300
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                                                                                                                                                  92 ----YICQTLDGALGGTVTLQLGYPPARPV-VSCQAADYENFSCTWSPSQ--ISGLPTRY
                                                                                                                                                                                                                                            41
                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                          SGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNY 123
                                                                                                                                                                                                                                 GRSVKLCC-----PGVTAGDPVSWFRDGEPKLLQGPDSGLGHELVLAQADSTDEGT--- 92
                                                                                                                                                                                                                                                                           GSSLQATCSIHGDTPGATA-EGLYWTFNG--RRLPSELSRLLNTSTLALALANLNGSRQQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                             1 Similarity
40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-422 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                          10.7%; Score 107.5; DB 2; 26.3%; Pred. No. 0.0046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Lebeau, B.; Dubois, S.; Moreau,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 112.5; DB 2; Pred. No. 0.0028;
                                                                                                                                                                                                                                                                                                                           Mismatches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human
                                                                                                                                                                                                                                                                                                                         67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270/3;
                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.F.; Bataille, R.; Minvielle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318/1; 358/1; 390/2; 418/1
                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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prolactin

receptor

long

form precursor, hepatoma and breast cancer cells

human

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163 DLGGSHQSPRL 173 : |: ||:| 207 NALGTSMSPQL 217

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Reywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;15-24/Domain: signal sequence #status predicted <SIG>
F;25-622/Product: prolactin receptor, long form #status predicted <MAT>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Expression cloning of a human granulocyte colony-stimulating A; Reference number: JH0329; MUID:91079757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Identification of a cDNA encoding a long A; Reference number: A40144; MUID: 90114212
A; Accession: A40144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:120
A;Map position: 5p13.3-5p13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-622 <BOU>
                                                                                                                                                                                                                                                                                                                                                                           ,628-653/Domain: transmembrane #status predicted <TRA>
,654-783/Domain: intracellular #status predicted <INT>
,93,128,134,389,474,579,610/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Experimental source: pauce: Reywords: glycoprotein; transmembrane protein; 1-24/Domain: signal sequence #status predicted <SIG>;1-24/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Larsen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:X55720; NID:g31698; PID:g31699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: JH0329; S21608
Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel,
Exp. Med. 172, 1559-1570, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 12-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-627/Domain: extracellular #status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: GDB:PRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Houtin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession:
         149
                                              115 GETFLHTNYSLK-YKLR---LVRSEXHMXGVP--
                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                                                                                                   83/Product: granulocyte colony-stimulating 27/Domain: extracellular #status predicted
                                                                                                                             59 GSRQQSGDNLYCHARDGS---ILAGSCLYYGLPPEKPFNISC-WSRNMKDLTCRWTPGAH 114
                                                                                                                                                                           34 PIVHLGDPITASCIIKQNCSHLDPEPQILWRLGAELQPGGRQQRLSDGTQESIITLPHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 ILAGSCLYYG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKY
                                                                                                                                                                                                                  2 PTILIGSSIQATCSIHGDTPGATAE-GLYWTFNGRRLPSELSRLLN--TSTLALALANIN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTY
                                                                                        HTQA----FLSCCLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLICQWEPGP-
-ETHLPTSFTLKSFKSRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLY-QNMGIWVQAE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.M.; Edery,
                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            colony-stimulating factor receptor D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-783 <LAR>
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDB:120315; OMIM:176761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ry, M.; Shirota, M.; Jolicoeur, C.; 1455-1461, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB:M31661; NID:g190361; PID:g190362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #sequence_revision 17-Jul-1992 #text_change 24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.18;
                                                                                                                                                                                                                                                                                          9.98;
                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101.5; DB 2;
Pred. No. 0.028;
3; Mismatches 22;
                                                                                                                                                                                                                                                                                          Score 100; DB 2;
Pred. No. 0.051;
                                                                                                                                                                                                                                                                   Mismatches .
                                         -HC---EPSLMPYPQGPGPLHSLX 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sims,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        form of prolactin receptor in human
                                                                                                                                                                                                                                                                                                               Length 783
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lesueur, L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor D7
                                                                                                                                                                                                                                                                                                                                                                                (Asn) (covalent)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                   26;
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••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #status predicted
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                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          factor receptor
                                                                                                                                                                           93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.; Park,
                                                                                                                                                                                                                                                                                                                                                                                #status
                                                                                                                                                                                                                                                                   11;
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                   A;Residues: 1-680,708-863 <LAR>
A;Cross-references: GB:X55721; NID:g31696;
A;Note: clone 25-1; placenta
                                                                                                                        A;Cross-references: GB:M59818; GB:M38025; NID:g183046; PID:g183047
A;Note: clone pHQ3
R;JARSen, A: Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; ScJ. Exp. Med. 172, 1559-1570, 1990
A;Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: A;Reference number: JH0329; MUID:91079757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  granulocyte colony-stimulating factor receptor precursor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               용
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                               A; Molecule type: mRNA
A; Residues: 1-680,708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contains: granulocyte colon
Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S. roc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990 ;Title: Three different mRNAs encoding human granulocyte;Reference number: A38252; MUID:91062348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ranulocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                            Reference number: A38252; MUID:91062348 Accession: C38252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title: Three different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 17-Mar-1999 Accession: C38252; A38252; JH0330; A46486; S68332; S21607 Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date: 14-Jun-199
                                                                                                                                                                                                                                                  Molecule type: mRNA
Residues: 1-680,708-863 <FU2>
                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                  Note: clones pHG11 and Accession: A38252
                                                                                                                                                                                                                                                                                                                                                                             Molecule type: mRNA
Residues: 1-863 <FUK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oc. Natl. Acad. Sci. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession:
                                                                                                                                                                                                                                                                                              tatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIVHLGDPITASCIIKQNCSHLDPEPQILWRLGAELQPGGRQQRLSDGTQESIITLPHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTLLIGSSLQATCSIHGDTPGATAE-GLYWTFNGRRLPSELSRLLN--TSTLALALANLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NALGTSMSPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTQA----FLSCCLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLICQWEPGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSRQQSGDNLVCHARDGS---ILAGSCLYVGLPPEKPFNISC-WSRNMKDLTCRWTPGAH 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -ETHLPTSFTLKSFKSRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLY-QNMGIWVQAE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type: mRNA: 1-771 <FUK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              granulocyte colony-stimulating factor, long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colony-stimulating factor receptor precursor (clone pHQ2) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 #sequence_revision 14-Jun-1991 #text_change 31-Oct-1997
                                                                                                                                                                                                                                                                                                                                     GB:M59820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB:M59819; GB:M38026; NID:g485363;
Nagata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.98;
                                                                                                                                                                                                                                                                                                                                                         GB:M38027; NID:g183048; PID:g183049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 100;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human granulocyte colony-stimulating
                                       PID:g31697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 771;
.05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149
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C;Accession: I45971
C;Accession: I45971
R;Scott, P; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A;Title: Molecular cloning of the bovine prolactin receptor and armaference number: I45971; MUID:93246019
                          A; Residues: 1-581 <SCO>
                                                                                                                                                                                                                                                                                                                                                                                                    밁
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A;Cross:references: GB:L02549; NID:g163617; PID:g163618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;628-653/Domain: transmembrane *status predicted <TMM>;654-863/Domain: intracellular *status predicted <INT>;93,128,134,389,474,579,610/Binding site: carbohydrate
                                                                                                                                                                                                                           Species: Bos primigenius taurus (cattle)
Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-863/Product: granulocyte colony-stimulating factor receptor, long 25-860,708-863/Product: granulocyte colony-stimulating factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Map position: 1p35-1p34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reference number: A46486; MUID:92091782 Accession: A46486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: sequence extracted from NCBI backbone (NCBIN:71484, NCBIP:71485) Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GDB:126430; OMIM:138971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: GDB:CSF3R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Residues: 855-863 <SET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-627/Domain: extracellular #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reference number: S68331; MUID:96132662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Experimental source: granul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -24/Domain: signal sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ross-references: GB:S71484; NID:g240883; PID:g240884
                                                                                                                                                                                                                                                                                actin receptor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               iu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, N
Blochem: Biophys. 324, 344-356, 1995
le: Extracellular domain of granulocyte-colony stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  words: alternative splicing; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                               207 NALGTSMSPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                             163 DLGGSHQSPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 -ETHLPTSFTLKSFKSRGNCQTQGDSILDCVPKDGQSHCCIPRKHLLLY-QNMGIWVQAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 GETFLHTNYSLK-YKLR---LVRSEXHMXGVP-----HC---EPSLMPYPQGPGPLHSLX 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 HTQA----FLSCCLNWGNSLQILDQVELRAGYPPAIPHNLSCLMNLTTSSLICQWEPGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 GSRQQSGDNLVCHARDGS---ILAGSCLYYGLPPEKPFNISC-WSRNMKDLTCRWTPGAH 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIVHLGDPITASCIIKQNCSHLDPEPQILWRLGAELQPGGRQQRLSDGTQESIITLPHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTLLIGSSLQATCSIHGDTPGATAE-GLYWTFNGRRLPSELSRLLN--TSTLALALANLN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234-269 CHANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S68332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 100; DB 2;
; Pred. No. 0.057;
27; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the human granulocyte colony-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor receptor,
                                                                                                                                    distribution
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Query Match Best Local Similarity

9.7%; 33.7%;

Score 98; Pred. No.

DB 2; 0.057;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.
Best Local Similarity 51.:
Matches 21; Conservative
                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                       Molecule type: protein
Residues: 41-58,'X',60-66;90-93,'X',95-96,'X',98-103,'X',105,'NX',108;150-164,'XX',167
Note: the amino end of the mature protein was blocked
Reywords: blocked amino end; 91/coprotein; transmembrane protein
1-24/Domain: signal sequence #status predicted <SIG>
25-616/Product: prolactin receptor 2 #status predicted <MAT>
235-258/Domain: transmembrane #status predicted <TMAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: A30304; A60380
Edery, M.; Jolicoeur, C.; Le
oc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: mRNA
Residues: 1-206 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    olactin receptor - human (fragment)
Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reference number: A57018; MUID:95286597
Accession: A57018
                                                                                                                                                                                                                                                                                                                                                                                                                    itle: Purification and partial sequence of the rabbit mammary gland prolactin receptorerence number: A60380; MUID:91146782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sidues: 1-616 <EDE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tle: Identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .ternate names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ross-references: GB:S78505; NID:g999114; PID:g999115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ecies: Oryctolagus cuniculus (domestic rabbit te: 07-Sep-1990 #sequence_revision 07-Sep-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  th, G.; Wells, J.A.

1001. Chem. 270, 13133-13137, 1995

11e: Prolactin receptor antagonists that inhibit the
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSS-references: GB:J04510; NID:g165669; PID:g165670
EJRS (M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
J. Blochem. 22, 1089-1095, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     actin receptor 2 precursor - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ference number: A30304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 MKDLTCRWTPGAHGETFLHTNYSLKY 127
88 PPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 KETFTCWWEPGADGG--LPTNYTLTY.64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
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                                                                          9.48;
illarity 50.08;
Conservative
                                                                                                                                                                                      ,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prolactin receptor, mammary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *sequence_revision 07-Sep-1990 #text_change 20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.; Levi-Meyrueis, C.; Dusanter-Fourt, 
J.S.A. 86, 2112-2116, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence analysis of a second form of prolactin MUID:89184578
                                                                     Score 95; DB 2; Length 616, Pred. No. 0.12; 2; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 95; DB 2; Length 206; Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPEKPKLVKCRSPG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I.; Petridou, B.; Boutin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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                                                                Gaps
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                                                                                                                                                                                                                                                                A;Cross-references: GB:M22957; NID:g200477; PID:g200478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pseudo-prolactin receptor precursor -
                                                                                                                                                                                                                                                                                                                                                         1; Accession:
                                                                                                                                                                   Query Match 9.48;
Best Local Similarity 33.08;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Title: Expression of multiple forms of the prolactin receptor in mouse liver Reference number: 157699; MUID:89261824
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Mus musculus (nouse mouse)
Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Aug-1996
                                                                                                                                                                                                                                                                                          Molecule type: mRNA
Residues: 1-97 <RES>
                                                                                                                                                                                                                                                                                                                               Status: preliminary; translated from GB/EMBL/DDB:
                                                                                                                             37
31 CRSPDKETFTCWWNPGSDGG--LPTNYSLTY 59
                                  CWSRNMKDLTCRWTPGAHGETFLHTNYSLKY 127
                                                                                                                  LPSELSRLLNTSTLALALANLNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNIS 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPGKPFIFKCRSPEKETFTCWWRPGADGG--LPTNYTLTY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                    Linzer, D.I.H.
                                                                                                                                                                 Conservative
                                                                           -LVLSISLLNG---QS----
                                                                                                                                                                                                                                                                                                                                                                                                                 1989
                                                                                                                                                                                   Score 95; DB 2;
Pred. No. 0.014;
                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse
                                                                                                                                                             20;
                                                                                                                                                                                                    Length 97
                                                                                                                                                             Indels
                                                                           PPGKPEIHK 30
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Search Job tir completed: September 16, 1999, 20:42:11

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein protein search, using sw model

September 17, 1999, 03:10:14; Search time 35.09 Seconds (without alignments)
149.840 Million cell updates/sec

Title:

Perfect score: Sequence:

US-09-037-657-29 1006 1 DPTLLIGSSLOATCSIHGDT.....SHQSPRLSKIXCPHTGCPGR 186

Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database : SwissProt_37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Score

Query Match Length DB

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Description

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50 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	X62646; G840817; M83336; G193592; MGI:96560; IL6ST. TE; PS00340; RECEP PF00041; fn3; 3. P40189; IBQU. TOR; TRANSMEMBRANE	SWISS-PROT entry en the Swiss In uropean Biolinforr by non-profit ied and this stat ies requires a li en email to li	DEVELOPMENTAL 6 OF GESTATION DURING THE RES SIMILARITY: BE SIMILARITY: BE ONE IG-LIKE DO SIMILARITY: CO	IT: HETERODIMER LLULAR LOCATION E SPECIFICITY: N, KIDNEY, LUNG T BAF-BO3, EXPR	FUNCTION: SIGNAL-TRA IL-6, LIF, OSM, CNTF SIGNAL TRANSMISSION. RESULTING IN THE FOR AND TRANSDUCES THE S EMBRYONIC DEVELOPMEN	FROM N.A. R; TISSUE-MAC 92291532. YOSHIDA K., YOSHIDA G., II cloning of II yp130, and L. 148:4066-4	LUS (MOUSE). ; METAZOA; CHOR SCIUROGNATHI;	(REL.	Ħ		7.1
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Best Local Similarity
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A BRAYO J., STAUNTON D., HEATH J.K., JONES E.Y.;

A BRAYO J., STAUNTON D., HEATH J.K., JONES E.Y.;

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A BRAYO J., STAUNTON D., HEATH J.K., JONES E.Y.;

A CREMBO J. 17:1665-1674(1998).

C -1- FUNCTION: SIGNAL-TRANSDUCING MCLECULE. THE RECEPTOR SYSTEMS FOR LITIATING COMPLEX, CONTROL OF LITIATING FOR INTIATING COMPLEX, CONTROL OF SINDLE SINDLES OF BIND IL-6. MAY HAVE A ROLE IN CONTROL OF THE SIGNAL DOES NOT BIND IL-6. MAY HAVE A ROLE IN CONTROL OF SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

C -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C -1- TISSUE SPECIFICITY: FOUND IN ALL THE TISSUES AND CELL LINES.

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101-FEB-1998 (REL. 37, LAST ANNOTATION UPDATE)
1NTERLEUKUN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA)
6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130)
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SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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SER-RICH. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEDLINE; 93052397.
WANG Y., NESBITT J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPEAT.
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EUKARYOTA; METAZOA; CHORDATA;
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5 SIGNAL TRANSDUCER)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEM IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INIT SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) CORESULTING IN THE FORWATION OF HIGH-AFFINITY IL-6 BINDING AND TRANSDUCES THE SIGNAL DOES NOT BIND IL-6. MAY HAVE A EMBRYONIC DEVELOPMENT (BY SIMILARITY).

SUBCULTURAL DOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND ENDOTHELIAL CELLS.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONE IG-LIKE DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEMBRANE;
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                                                                                                                                                                                                                                                       FIBRONECTIN TYPE-III
                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                         FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                          IG-LIKE C2-TYPE DOMAIN FIBRONECTIN TYPE-III.
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AE; MURINAE; RATTUS
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Lon of the ra
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                                                                                                                     ALTERNAI
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                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
LEUKEMIA INHIBITORY FACTOR RECEPTOR PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KING J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARING D.F., COSMAN D., BECKMANN F. Leukemia inhibitory factor receptor is """" transducer, gp130.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "ISSUE-PLACENTA
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                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE IG-LIKE DOMAIN.
SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 PTLLIGSSLQATCSIHG----DTPGATAEGLYWTFNGRRLPSELSRLLNTSTLALALANLN
                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS MAY ARISE BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HETERODIMER COMPOSED OF LIFE AND GP130 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: SIGNAL-TRANSDUCING
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                                                                                                                            GLYCOPROTEIN;
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        POTENTIAL.
                                                                                                                                                                                                                                  is not removed.
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                                  CYTOPLASMIC (POTENTIAL)
BY SIMILARITY.
                                                             EXTRACELLULAR POTENTIAL.
                                                                                        LEUKEMIA
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4; Mismatches 72;
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                                                                      INHIBITORY FACTOR RECEPTOR LULAR (POTENTIAL).
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                                                                                                                         IMMUNOGLOBULIN FOLD; SIGNAL
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                                                                                                                                                                  MEDLINE; 92007727.
GEARING D.P., THUT C.J., VANDENBOS T., GIMPEL S.D., KING J., PRICE V., COSMAN D., BECKMANN M.P.;
"Leukemia inhibitory factor receptor is structurally IL-6 signal transducer, 9p130.";
                                                                                                                                                                                                                                                                                                01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
LEUKEMIA INHIBITORY FACTOR RECEPTOR PRECURSOR
                                                                                                                                                                                                                                                                                                                                        LIFR_MOUSE P42703;
                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
RODENTIA; SCIUROGNATHI; MURIDA
                                                                                                                                                                                                              SEQUENCE FROM N.A. (SECRETED FORM).
MEDLINE; 92007727.
                                                                                                                                                                                                                                                                             LIFR.
                                                                                                                                                                                                                                                                                      RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                         111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258
TOMIDA H., YAMAMOTO-YAMAGUCHI Y., HOZUMI M.;
"Three different cDNAs encoding mouse D-factor/LIF receptor.";
"EIOCHEM. 115:557-562(1994).
-i- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON P.
WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIV
                                                                                                                                                                 EMBO
                                                                                                                                                                                                                                                                                                                                                                                                      355
                                                                                                                                                                                                                                                                                                                                                                                                                                            298
                                                                                "Pregnancy associated increase receptor in mouse liver."; FEBS LETT. 334:193-197(1993).
                                                                                                                     MEDLINE; 94039833
                                                  MEDLINE: 94334302
                                                            SEQUENCE FROM N.A.
                                                                                                             TOMIDA M., YAMAMOTO-YAMAGUCHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                51
                                                                                                                                  EQUENCE FROM N.A. (SECRETED FORM).
TRAIN-ICR; TISSUE-LIVER;
                                                                                                                                                              ) 5. 10:2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 23.4
36; Conservative
                                                                                                                                                              nal transducer, gp
10:2839-2848(1991)
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                                                                                                                                                                                                                                                MURIDAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 115; DB 1; Pred. No. 0.0013; 8; Mismatches 4
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AE; MURINAE;
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 MOLECULE. MAY HAVE A COMMON PATHWAY INHIBITS THE BIOLOGICAL ACTIVITY OF
                                                                                                     mRNA for s
                                                                                                                                                                                                                                                                                                                                                    1092
                                                                                                                                                                                   is structurally related to
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                                                                                                                                                                                                                                                MAMMALIA;
MUS.
                                                                                                      soluble
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1097;
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                                                                                                      D-factor/LIF
                                                                                                                                                                                                                                                          EUTHERIA;
                                                                                                                                                                                                        DELANEY P.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENV
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Matches 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- ALTERNATIVE PRODUCTS: THE SECRETED MAY ARISE BY ALTERNATIVE SPLICING.
-I- SIMILARITY: BELONGS TO THE IMMUNOG
                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
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CARBOHYD
CARBOHYD
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VARSPLIC
SEQUENCE
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EMBL; S73495; G688384; -.
EMBL; D26177; G825506; -.
EMBL; D17444; G441494; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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DISULFID
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                                                                                                                                                                                                                     CARBOHYD
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PROSITE; PS00241; RE
                                                                                                                                                                                   CARBOHYD
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                                            253
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                     59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ONE IG-LIKE DOMAIN.
SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION:
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TISSUE SPECIFICITY: PLACENTA, LIVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIF BY BLOCKING ITS BINDING
                     GSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPG
                                                         DPTLLIGSSLQATCSIHGDTPGATAEGLYWTFNGRRLPSELSRLLNT--STLALALANIN 58
VS-ENSGINIIFIIDDD--VYGIVVFAGYPPDVPQKLSCETHDLKEIICSWNPG
                                            DKVVLAGSNMTICCM----SPTKVLSG---
                                                                                          Similarity 25., 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEMBRANE;
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LAR LOCATION: TYPE I MEMBRANE PROTEIN. T
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                                                                                                                                                POTENTIAL.
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AP -> EA (IN SECRETED FO MISSING (IN SECRETED FO JUNE 1) AM; 07DC092F CRC32;
                                                                                          27;
                                                                                                    Score 112.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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                                                                                           Mismatches
                                             ----QIGNTLRPLIHLYGOTVAIHILNIP
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                                                                                                                                                                                                                                                                                                                                                                                                          INHIBITORY FACTOR RECEPTOR.
JULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND THE
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                                                                                                      .0024;
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                                                                                           41;
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                                                                                                                 Length 1092;
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RESULT 6

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RESULT 7
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01-AUG-1990
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                          MAIN
                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00241; PROSITE; PS00340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions a modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOMERS W., ULTSCH M., DE "The X-ray structure of a NATURE 372:478-481(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VEI
PRIMATES; CATARRHINI; HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OOUTIN J.-M., EDERY M., SHIROTA M., JOLICO
NII S., GOULD D., DUIANE J., KELLY P.A.,
'Identification of a CDNA encoding a long
In human hepatoma and breast cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 90114212.
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P16471;
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                                                                                       15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tities requires a license agreement ( send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                           ILAGSCLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1BP3; 2
176761;
                                                                             LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTY
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                                                                                                                                                               Similarity
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                                                                                                                                              Conservative
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(REL. 15, LAST SEQUENCE UP
(REL. 37, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G190362;
        STANDARD;
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RECEPTOR_CYTOKINES_2;
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                                                                                                                                                                                                                    PIBRONECTIN TYPE-III.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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6924E155 CRC32;
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                                                                                                                                           Score 101.5;
Pred. No. 0.01
3; Mismatches
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        PRT;
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REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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MEDLINE; 97331327. ANAC
YAMASAKI K., NAITO S., ANAC
"Solution structure of an a
motif of the granulocyte oc
interaction with ligand.";
NAI: STRUCT. BIOL. 4:498-5
                                                                                                                                                                                                              LAYTON J.E., IARIA J., SMITH D.K., TREUTLEIN H.R.;
"Identification of a ligand-binding site on the granulocyte colony-
stimulating factor receptor by molecular modeling and mutagenesis."

J. BIOL: CHEM. 272:29735-2974(1997)

-I- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G.
CCE). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITIO
                                                                                                                                                                   -!- SUBUNIT: DIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 92091/02.
SETO Y., FUKUNAGA R., NAGATA S.
"Chromosomal gene organization
"Chromosomal gene organization.";
                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99062;
01-FEB-1995
01-FEB-1995
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUKUNAGA R., ISHIZAKA-IKEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
FUKUNAGA
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PRIMATES; C
                                                                                                                                                                                                                                                                                                                               3D-STRUCTURE MODELLING OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MBO J. 10:2855-2865(1991).
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encodes a secreted protein.";
J. EXP. MED. 172:1559-1570(1990);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LARSEN A.,
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EDLINE; 91011257.
ARSEN A., DAVIS T.,
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OF THE RECEPTOR.

OF THE RECEPTOR.

OF THE RECEPTOR.

ONE OR SEVERAL FORMS HAVE BEEN FOUND IN MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES. THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE GSCFR-3 FORM IS HIGHLY EXPRESSED IN PLACETIA U937 CELLS. THE ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS, GCSFR-1 (SHOWN UNDER), GCSFR-2, GCSFR-3 AND GCSFR-4/D7, ARE PROBABLY PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THEY DIFFER IN THEIR C-
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                                                                                                                                                                                                    CSF). IN ADDITION IT MAY FU
EVENTS AT THE CELL SURFACE.
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148:259-266(1992).
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L. 31, LAST SEQUENCE UPDATE)
L. 37, LAST ANNOTATION UPDATE)
TTMTLATING FACTOR RECEPTOR P
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PROSITE; PS00340; RECEPTOR_CYTOKINES_2; 1.
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SEQUENCE
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SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00041; fn3; 3.
TOR; TRANSMEMBRANE; GLYCOPROTEIN; IMMUNOGLOBULIN FOLD;
T; ALTERNATIVE SPLICING; 3D-STRUCTURE.
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836 AA;
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TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
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IG-LIKE C2-TYPE DOMAIN.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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PDPAHSSLGSWYPT MEEDARQLPGLGTPFITKLTVLEEDE
KKPYPRESHNSSETCGLPTLVGTYVLGGDPRAVSTQPOSQS
GTSDQYLYGQLLGSPTSPGPGHYLTVLQGDPRAVSTQPOLGS
SYENLWFQASPLGTLYTPAPSQEDDCYFGPLLNFPLLQGIR
VHGMEALGSF -> APTGRIPSGQVSQTQLTAAWAPCCPQS
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                                     VHGMEALGSE -> APTGRIPSGQVSQTQLTÄAWAPGCPQS
WRRMPSSCPALARHPSPSSQCWRRMKRSRCPGSPITAQRPV
ASPLWSRPMCSRGTQEQFPPSPNPSLAPAIRSFMGSCWAAP
                          QAQGQGTISAVTPLSPSWRASPPAPSPMRTSGSRPAPWGPW
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AGPPRRSAYFKDQIMLHPAPPNGLLCLFPITSVL
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Best Local S
Matches 51
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BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
EUKARYOTA; MUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE;
                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROLACTIN RECEPTOR PRECURSOR (PRL-R).
DOMAIN
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DISULFID
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SCOTT P., KESSLER M.A., SCHULER L.A.;

Molecular cloning of the bovine prolactin receptor and
of prolactin and growth hormone receptor transcripts in
utero-placental tissues.";

MOL. CELL. ENDOCRINOL. 89:47-58(1992).
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                                                                                                                                                                                                                                                      PFAM; PF00041; HSSP; P14787;
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                                                                                                                                                                                                                                 TRANSMEMBRANE;
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                                                                                                                                                                                                                                 GLYCOPROTEIN;
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Pred. No. 0.
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                                                                                                    EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                 PROLACTIN
     BY SIMILARITY.
                                                  FIBRONECTIN TYPE-III.
                                                                                                                                                                                                            POTENTIAL
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                                                                                                                                                                                    RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF RECEPTORS
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SEQUENCE
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01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDAT
PROLACTIN RECEPTOR PRECURSOR (PRL-R).
                                                                                                                                                                  use by non-profit institutions a modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA; METAZOA; CHORDATA; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RABIT
                                                                                                     PIR; A30304; A30304.
PDB; 1AN3; 03-DEC-97
                                                                                                                         EMBL; J04510; G165670; -.
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                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a coefficient the Swiss Institute of Bioinformatics and the EMBL
                          MAIN
                                       CHAIN
                                                                                                                                                           entities requires a
                                                                                                                                                                                                                                                                                          PROTEINS 27:459-468(1997).
                                                                                                                                                                                                                                                                                                               "HOMOLOGY modeling
                                                                                                                                                                                                                                                                                                                                      3D-STRUCTURE MODELLING MEDLINE; 97248733.
                                                                                                                                                                                                                                                                                                                                                                                     EDERY M., JOLICOEUR C., LEVI-MEYRUEIS C., DI
PETRIDOU B., BOUTIN J.M., LESUEUR L., KELLY
"Identification and sequence analysis of a a
receptor by molecular cloning of complementa
mammary gland":
                                                                                                                                                                                                                                                                                                                                                                                                                             WEDLINE; 89184578.
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ROC. NATL. AC
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                                                                                                                                                                             European Bioinformatics Institute.
by non-profit institutions as k
                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                       PROLACTIN
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29; Conserv
                                                                             PS00340; RECEPTOR_CYTOKINES_1;
PS00340; RECEPTOR_CYTOKINES_2;
                                                          TRANSMEMBRANE;
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33.78;
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                                                      GLYCOPROTEIN; SIGNAL; REPEAT; 3D-STRUCTURE.
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POTENTIAL.
COECAOA2
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                   BY SIMILARITY.
PROLACTIN RECEPTOR
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1.03;
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PIR; JL0145; JL0145.
PIR; S14543; S14543; S165A.
MGD; MGI-105304; RECEPTOR_CYTOKINES_1;
PROSITE; PS00340; RECEPTOR_CYTOKINES_2;

PF00041; fn3; 1 PF00047; ig; 1. P16471; 1BP3.

TRANSMEMBRANE;

GLYCOPROTEIN; IMMUNOGLOBULIN FOLD; SIGNAL

EMBL; EMBL; PIR;

X51975; G49726; -. X53802; G52693; -.

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SEQUENCE
                                                                                                       use by non-profit institutions modified and this statement is not entities requires a license agreem or send an email to licenseelsb-si
                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                   STRAIN-C3H, TISSUE-LIYER;
FIORILLO M.T., CITIBERTO G., DENTE L.;
SUBMITTED (JUL-1990) TO EMBL/GENBANK/DDBJ DATA BANKS.
-I- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6.
                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                  particle gene product at its cytoplasmacytomagenesis.";
j. EXP. MED. 171:2001-2009(1990)
                                                                                                                                                                                                                                                                                                                                                 STRAIN-BALB/C; TISSUE-SPLEEN; MEDLINE; 90278354.
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                      Functional murine interleukin
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20; Conser
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(REL.
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BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                 19, CREATED)
23, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
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2; Mismatches
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IMMUNOGLOBULIN SUPERFAMILY.
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No. 0:064;
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MUS.
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Matches 34
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D1-OCT-1996 (REL. 34, CREATED)

O1-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

O1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR ('KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2)
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                      CROSIER P.S., LEWIS P.M., HALL L.R., VITAS M.R. BEIER D.R., WOOD C.R., CROSIER K.E.;
"Isolation of a receptor tyrosine kinase (DTK) cells: structure, genetic mapping and analysis GROWTH FACTORS 11:125-136(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 94193774.
MARK M.R., SCADDEN D.T.,
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                                STRAIN-BALB/C; TIS
MEDLINE; 95240399
                                                                                                         "Structure, expression, and active related receptor tyrosine kinase. ONCOGENE 9:2567-2578(1994).
                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  ARK M.R., SCADDEN D.T., WANG Z., GU Q., GOD RSE, a novel receptor-type tyrosine kinase is expressed at high levels in the brain."; r. BIOL. CHEM. 269:10720-10728(1994).
                   SCHULZ
                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S--DTGDYL-CSLNDH--LYGTVPLLYDVPPEEP-KLSCFRKNPLYNAICEWRPSS
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                                                                                                                                                                 GORE M., LEMKE G.;
                                                                                                                                                                                   94336210
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and expression
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                   PAULHIAC C., LEE L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                     TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
460
357
385
460
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92
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173
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THI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50454
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                                                                                                                                                                                                                                                                                                                CROSIER K.E.;
                                                                                                                                      and activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥.
EE L., ZHOU R.;
analysis of ty
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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BY SIMILARITY.
POTENTIAL.
POTENTIAL.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A -> R (IN REF. 2)
0B9F5F46 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG-LIKE C2-TYPE POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    880
                                                                                                                                                  of,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
0.072;
                                                                                                                                                  Tyro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GODDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAMMALIA;
MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTOR ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                  ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 460
                                                                                                                                                                                                                                                                             from embryonic stem
of expression.";
   murine
                                                                                                                                                    മ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homology
                                                                                                                                                                                                                                                                                                                                     MORRIS C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                  neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GODOWSKI P.J.;
ology to Axl/Ufo,
                                                                                                                                                    adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
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Isolation

Query Match Best Local S Matches 41

Similarity

9.0%;

Conservative

18;

Mismatches

53 ;

Indels

74;

Gaps

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PFAM; PF00041;
PFAM; PF00047;
PFAM; PF00069;
HSSP; P11362; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA -I- FUNCTION: MAY BE INVOLVED IN CELL ADHESION IN THE CENTRAL NERVOUS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor tyrosine kinase preferentially expressed BRAIN RES. MOL. BRAIN RES. 28:273-280(1995).
                                                             CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U05683; G469519;
EMBL; U18933; G622983;
EMBL; X78103; G473097;
EMBL; U18342; G687626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE
                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:104294; TYRO3
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_DOM;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                             ONIB_AND
                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                            RECEPTOR; GLYCOPROTEIN; TYROSI
TRANSFERASE; PHOSPHORYLATION;
                                                                                                                                CARBOHYD
                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                   OMAIN
                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCRELIULAR LOCATION: TYPE I MEMBRANE PROTEIN TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND OTHER TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN THE CENTRAL NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR DOMAINS
                                                                                                                                                                                                                                                                                                                                                            pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                      626; ALT_INIT.
019943; -.
                                                                181
230
230
356
370
                                                                                                                                                              440
880
200
200
301
785
522
540
676
                                                                                                                                                                                                                                                                                                                             TYROSINE-PROTEIN KINASE; ATP-BINDING ATION; TRANSMEMBRANE; SIGNAL; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONTAINS 2
                                            3
                                                                                              POTENTIAL.
POTENTIAL.
                                                                                                                                                                         ATP (BY SIMILA
ATP (BY SIMILA
BY SIMILARITY.
Score 91; I
                                                                          POTENTIAL.
                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE DOMAIN.
IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                  POTENTIAL.
TYROSINE-PROTEIN KINASE RECEPTOR TYRO3.
EXTRACELLULAR (POTENTIAL).
                                                                                                                              PHOSPHORYLATION (AUTO-)
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                   FIBRONECTIN TYPE-III.
                                                                                                                                                                                    (BY SIMILARITY). (BY SIMILARITY).
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IN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                           KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no
                                           REF. 3).
REF. 3).
CRC32;
 DB 1;
0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROCESSES,
            Length 880;
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                                                                                                                                                                  SIMILARITY).
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REAL STREET STRE
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GCSR_M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCSR_MOUSE
P40223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LT 12
MOUSE
                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed, entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UF
15-JUL-1998 (REL. 36, LAST ANNOTATION
GRANULCCYTE COLONY STIMULATING FACTOR
                                            PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PROSITE; PS00340; RECEPTOR_CYTOKINES_2; PFAM; PF00041; fn3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Expression cloning of a stimulating factor."; CELL 61:341-350(1990).
                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                       or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSF3R OR CSFGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 225-333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUKUNAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nteraction with ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMASAKI K., NAITO S., ANAGUCHI H., OHKUBO T., Solution structure of an extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: DIMER (PROBABLE).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: FOUND IN BONE MARROW.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPE
ONE IG-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-
ADDITION IT MAY FUNCTION IN SOME ADHESION
THE CELL SURFACE.
                                                                                                                                                                                                                                                                                                                                                                    ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through reen the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restr
                                                                                                                  MGI:88533; CSFGR
                                                                                                                                                                                           , M58288; G1934
A34898; A34898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPSPYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tion structure of an extracellular domain containing the WSxWS
of the granulocyte colony-stimulating factor receptor and its
                                                                                                                                                                                                                                                                       an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R., ISHIZAKA-IKEDA E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97331327
                  TRANSMEMBRANE;
                                                                                                                                       22-OCT-97.
22-OCT-97.
                                                                                                                                                                                                                                                                    email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS. BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
               GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERTEBRATA;
AE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SETO Y.,
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ON UPDATE)
OR RECEPTOR PRECURSOR (G-CSF-R).
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                                                                                                                                                                                                                                                                                         (See http://www.isb-sib
             IMMUNOGLOBULIN
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MUS.
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               FOLD;
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Best Local Similarity
Matches 45; Conserv
                 MEDLINE; 91060602.

BAUMANN M., BAUMANN H., FEY G.H.;

"Molecular cloning, characterization a rat liver interleukin 6 receptor.";

Tat liver interleukin 6 receptor.";

BIOL. CHEM. 265:19853-19862(1990).
                                                                                                                                                               P22273;
01-AUG-1991
01-FEB-1995
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
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DOMAIN
                                                                                                          RATTUS NORVEGICUS (RAT)
EUKARYOTA; METAZOA; CHO
RODENTIA; SCIUROGNATHI;
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CARBOHYD
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DOMAIN
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CHAIN
                                                                              SEQUENCE FROM N.A. STRAIN-FISHER 344;
                                                                                                                                                 01-AUG-1991 (REL. 19, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
INTERLEUKIN-6 RECEPTOR ALPHA CHAIN PRECURSOR
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                                                                                                                                                                                                                                                                                                                    TFLHTNYSLKYKLRLVRSEXHMXGVPHC-----
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                                                                                                                                                                                                                                                                                                                                                                               PVVRLGDPVLASCTISPNCSKLDQQAKILWRLQDEPIQPGDRQHHLPDGTQESLITLPHL
                                                                                                                                                                                                                                                                                                THIPTSFILKSFRSRADCQYQGDTIPDCVAKKRQNNCSIPRKNLLLY-QYMAIWVQAENM
                                                                                                           ; METAZOA; CHORDATA; SCIUROGNATHI; MURIDA
                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 23.8
Conservative
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                                                                                                                                                                                                      STANDARD;
                                                                              TISSUE-LIVER
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23.8%; Pre
28;
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                                                                                                           MURIDAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 90.5; D
Pred. No. 0.26
28; Mismatches
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BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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GRANULOCYTE COLONY STIMULATING RECEPTOR.
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                                                                                                           VERTEBRATA;
AE; MURINAE;
                                                                                                                                                                                                      PRT;
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                                                and
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                                                functional
                                                                                                          MAMMALIA;
RATTUS.
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Best Local
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Q90374;
Q1-NOV-1997
Q1-NOV-1997
15-JUL-1998
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-I- FUNCTION: PART OF THE RECEPTOR.FOR INTERLEUKIN 6. BINDS WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
-I- SUBGUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00241; RECEPTOR_CYTOKINES_1; PROSITE; PS00340; RECEPTOR_CYTOKINES_2;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M58587; G204922; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                          01-NOV-1997 (REL: 35, CREATED)
01-NOV-1997 (REL. 35, LAST SENGENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
PROLACTIN RECEPTOR PRECURSOR (PRL-R).
                                                        COLUMBA LIVIA (DOMESTIC PIGEON) EUKARYOTA; METAZOA; CHORDATA; V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRANSMEM
          SEQUENCE FROM N.A.
TISSUE-CROPSAC;
                                             NEOGNATHAE; COLUMBIFORMES; COLUMBIDAE; COLUMBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGNAL
                                                                                                                                                                                                                                                                 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                   TLLIGSSLQATCSIHGDTPGATAEG----LYWTFNGRRLPSELSRLLNT--STLALALANL 57
                                                                                                                                                                                                                 NDT----GHYLCFLDDH--LVGTVPLLVDVPPEEP-KLSCFRKNPLVNAFCEWHPSS 134
                                                                                                                                                                                                                                         NGSRQQSGDNLVCHARDGSILAGSC-LYVGLPPEKPFNISCWSRN-MKDLTCRWTPGA 113
                                                                                                                                                                                                                                                                TSLPGATVTLIC------PGKEAAGNATIHWVYSGSQ-----SREWTTTGNTLVLRAVQV 84
                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                                                                                            Similarity
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                                                          METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA;
                                                                                                                                                                                                                                                                                                                                                                            462
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                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                          Score 89;
Pred. No.
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POTENTIAL.
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B9BAFCC8
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BY SIMILARITY.
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SLVGSKSVGKTLSPGTQVTTCCNSSFDTDLYGQRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                       Length 462
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DISULFID
CARBOHYD
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Q28235;
01-NOV-1997
01-NOV-1997
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PROLACTIN RE
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modified and this statement is not received
entities requires a license agreement (
or send an email to license@isb-sib.ch)
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ENDOCRINOLOGY 135:269-276(1994).
ENDOCRINOLOGY THIS IS A RECEPTOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning, expression, a
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HSSP; P16471; 1BP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: TYPE
-1- SIMILARITY: BELONGS TO THE
-1- SIMILARITY: CONTAINS 4 FIBE
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                                                                                                                                              EUKARYOTA; METARTIODACTYLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           CEREL
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                                                                                                                                                                               CERVUS ELAPHUS (RED EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231
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34507 MW;
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                                                                                                                                                    RUMINANTIA;
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BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEMBRANE; GLYCOPROTEIN; SIGNAL; REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                35, CREATED)
35, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE
                                                                                                                                                                                                                                                                    PRECURSOR
                                                                                                                                                                                                           DEER)
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                                                                                                                                                                               CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.8%;
                                                                                                                                                 PECORA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 89; DB; Pred. No. 0.36
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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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SEQUENCE FROM N.A.

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Query Match 8.9
Best Local Similarity 40.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X94953; E218406;
PROSITE; PS00241; RECEPP
PROSITE; PS00340; RECEPP
PFAM; PF00041; fn3; 2.
HSSP; P14787; 1AN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KELLY P.A.,
                                                                                                                                                    CARBOHYD
CARBOHYD
SEQUENCE
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DISULFID
DISULFID
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
:- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
:- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                     18 NASTLNGQS-----PPGKPKIIKCRSPGKEIFTCWWEPGSDGG--LPYNYTLTY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the prolactin receptor gene during the breeding and geasons in red deer (Cervus elaphus): evidence for the
                                                                                                                                                                                                                                                                                                                                                                                                                                  41; RECEPTOR_CYTOKINES_1; 1.
40; RECEPTOR_CYTOKINES_2; 1.
                                                                                      8.8%;
                                                                                                                                                       46
86
89
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233
65159 MW;
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                                                                      Score 88.5; DB Pred. No. 0.26; S; Mismatches
                                                                                                                                                      POTENTIAL.
POTENTIAL.
721F0366 CRC32;
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BY SIMILARITY.
                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                             PROLACTIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                              FIBRONECTIN TYPE-III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as its content
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Search completed: September 17, 1999, 03:10:15
Job time: 295 sec

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1006
1 DPTLLIGSSLQATCSIHGDT.....SHQSPRLSKIXCPHTGCPGR 186
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165.996 Million cell updates/sec
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                 GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.
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sp_unclassified:*
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002671
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1 064151
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046561
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        002671 sus scrofa
093404 oreochromis
Q64151 mus musculu
                                                                                                                                                                                                   018880 bos taurus
Q16354 homo sapien
015051 homo sapien
                                                   044924 drosophila
                                                                                                                                                             Q64385 mus 1
P70225 mus 1
Q00343 mus 1
Q99650 homo 1
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057519 xenopus lae
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)76281 drosophila
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RESULT 057519 ID 057 AC 057 DT 01-DT 01-DT 01-DT 01-DT 6P1

O57519 PRELIMINARY; PRT; 881 AA. 057519; O1-JUN-1998 (TrEMBLrel. 06, Created) O1-JUN-1998 (TrEMBLrel. 06, Last sequence update) O1-MAY-1999 (TrEMBLrel. 10, Last annotation update)

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1 DPTLLIGSSLOATCSIHGDTBGATAEGLYWTENGRRLPSELERLNTSTLALALANLANG	PFAM: PF00041; fn3; 2. Signal. Signal. 1 37 POTENTIAL. CHAIN. 38 422 CYTOKINE-LIKE FACTOR-1. CHAIN. SEQUENCE 422 AA; 46301 MW; 877F9BC9 CRC32; SEQUENCE 422 AA; 46301 MW; 877F9BC9 CRC32; Sequery Match Best Local Similarity 84.5%; Pred. No. 2.7e-62; Matches 125; Conservative 4; Mismatches 13; Indels 6: Ga	Homo sapiens (Human). Eukaryota; Metazoa; Chord Eutheria; Primates; Catar [1] SEQUENCE FROM N.A. ELSON G.C.A., GRABER P., MENOUD L.N., WELLS T.N.C. "CLF-1, a Novel Soluble P Cytokine Type-I Receptor J. Immunol. 0:0-0(1998).	ປາເກ	7.4 262 4 043561 7.4 233 4 043919 043919 h 7.4 958 4 Q92920 Q92920 h ALIGNMENTS	78.5 7.8 917 11 060625 mus mus 1 78 7.8 1299 4 015179 015179 bomos sap 2 77.5 7.7 270 2 P76995 3 77.5 7.7 1299 4 092823 025806 drosophi 5 77 7 127 12 P89532 025306 02580 homo sap 7 7 6.5 7.6 1404 4 015080 015080 homo sap 7 7 6.5 7.6 2222 5 097394 097394 drosophi 8 7 7 7 7 12 081195 060500 homo sap 9 7 7 12 081195 060500 homo sap 1 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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Best Local
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Submitted (JAN-1998) to the EM
EMBL; AF041845; AAAC03531.1; -
FFAM; PF00041; fn3; 4
SEQUENCE 881 AA; 99003 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1996) to the IEMBL; U64198; AAB36675.1; -
PFAM; PF00041; fn3; 3
SEQUENCE 862 AA; 97134 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRESKY D.H., YANG H.,
GATELY M.K., GUBLER U
Submitted (JUL-1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL-12 RECEPTOR BETA2.
Homo sapiens (Human).
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    194
                                               156
                                                                                                                               105 LTCRWTPGAHGETFLHTNYSLKYKLRLVRSEXHMXGVPHCEPSLMPY------PQGP-
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Eukaryota; Metazoa; Chordata; Crania
Batrachia; Anura; Mesobatrachia; Pip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
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SNFTAKVTAVNSLGSSSSLP
                                                                                VACTWERGR--DTHLYTEYTLQ-----LSGPKNLTWQKQCKDIYCDYLDFGINLTPESPE 193
                                                                                                                                                                                                                                                              ILLGSTVNITCSL-----KPRQGCFHYSRRNKLILYKFDRRINFHHGHSLNSQVTGLPL
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                                                                                                                                                                                 GTTLFVCKLACINSDEIQ---
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                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
43; Conser
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                                          -GPLHSLXDLGGSHQSP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 03, (TrEMBLrel. 08,
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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97134 MW;
                                                                                                                                                                                                                                                                                                                                                                                       11.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MINETTI L.J., CHUA A.O., NABAVI N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                  36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                Score 110.5; DB Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 167.5;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5FE4FBD5 CRC32;
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                                                                                                                                                                         -----ICGAEIFVGVAPEQPQNLSCIQKGEQGT 140
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                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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                                                                                                                                                                                                                                                                                                                                                             62;
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 862;
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                                                       Query Match
Best Local S
Matches 39
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Best Local
                                                                                                                     "Structure of the mouse oncostatin M (OSM) receptor: molecular cloning of the OSM receptor beta subunit."; submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AB015978; BAA33725.1; -. PFAM; PF00041; fn3; 3.
SEQUENCE 970 AA; 110070 MW; 0D17AD4B CRC32;
                                                                                                                                                                                                                                                              OSMR.
Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata;
                                                                                                                                                                                                                                                                                                          01-NOV-1998 (Tremblrel 08, 01-NOV-1998 (Tremblrel 08, 01-MAY-1999 (Tremblrel 10, ONCOSTATIN M RECEPTOR BETA.
                                                                                                                                                                                                                                                                                                                                                                 088821;
                                                                                                                                                                                                             TANAKA M., HARA T., COPELAND N.G., GILBERT D.J.,
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
    154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oncostatin M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 DKVLEEGSNV-TICLMYGQNVYNVSCKLQDEP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 98252923.
LINDBERG R.A., JUAN T.,
FLETCHER F.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          254 WEPGV--DITLIWRKORFQNYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 WTPGAHGETFL----HTNYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 VFLS------DTGTNINCQATKGPKRIFGTVLFVSKVLEEPKNVSCETRDFKTLDCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 LALALANINGSROOSGDNIVCHARDG-SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DPTLLIGSSLQATCSIHG------DTPGATAEGLYWTFNGRRLPSELSRLLNTST
 DKVLEEGSNV-TICLMYGQNVYNVSCKLQDEP---
                             DPTLLIGSSLQATCSIHG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF058805; AAC40122.1;
                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and characterization of a specific
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                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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AA; · 110229 MW;
                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                   10.7%;
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                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
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Last annotation updat
                                                                  Score 108;
Pred. No. (
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Pred. No. 0.
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                                                     Mismatches
                                                                                                                    0D17AD4B CRC32
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                        -DTPGATAEGLYWTFNGRRLPSELSRLLNTST 49
                                                                                                                                                                                                                                                                                                                                                                            970
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                                                                  0.0031;
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· IHGEQLDSHVSLLKLNNV 202
                                                                                                                                                                                                             JENKINS N.A.,
                                                                           Length 970;
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                                                    Indels
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Mus.
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                                                 Gaps
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Best Local
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                           01-AUG-1998
01-AUG-1998
01-MAY-1999
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01-NOY-1996 (TIEMBLIEL 0
01-NOY-1996 (TIEMBLIEL 0
01-NOY-1998 (TIEMBLIEL 0
01-NOY-1998 (TIEMBLIEL 0
INTERLEUKIN-11 RECEPTOR.
                                                                                             070535
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EMBL; Z38102; CAA86224.1
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                   145 LTSYRKKTVLGADSQRRSPSTGP--WPCPQDP 174
                                                                                                                                                                                               124 SLKYKLRLVRSEXHMXGVPHCEPSLMPYPQGP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IINVIELLE S., JACQUES Y.;
Molecular cloning of two isoforms of a receptor mematopoietic cytokine interleukin-11,";
slood 86:2534-2540(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             iomo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INVIELLE S
                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDLINE; 95399754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE OF 3-390 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AN LEUVEN F., STAS L.,
abmitted (SEP-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSUE-MUSCLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EREL M., SOREL M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50
                                                                                                                                                                                                                           ----YICQTLDGALGGTVTLQLGYPPARPV-VSCQAADYENFSCTWSPSQ--ISGLPTRY 144
                                                                                                                                                                                                                                                          SGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNY 123
                                                                                                                                                                                                                                                                                         GRSVKLCC-----PGVTAGDPVSWFRDGEPKLLQGPDSGLGHELVLAQADSTDEGT---
                                                                                                                                                                                                                                                                                                                          GSSLQATCSIHGDTPGATA-EGLYWTFNG--RRLPSELSRLLNTSTLALALANLNGSRQQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEPGV - - DTTLTWRKQRFQNYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTPGAHGETFL----HTNYSL 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LALALANINGSROOSGDNIVCHARDG-SILAGSCLYVGLPPEKPENISGWSRNMKDLTCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U32323; AAB36491.
                                                                                                                                                                                                                                                                                                                                                              40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOV-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOREL M., DUBOIS
         (TIEMBLrel. 07, Created)
(TIEMBLrel. 07, Last sequence update)
(TIEMBLrel. 10, Last annotation updat.)
HIBITOR FACTOR RECEPTOR ALPHA-CHAIN.
                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAA86570.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            45222 MW;
                                                                                                                                                                                                                                                                                                                                                                             10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEBEAU B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HILLIKER C., MIYAKE Y., GOSSLER A.; the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              24;
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S
                                                                                                                                                                                                                                                                                                                                                           Score 107.5; DB
Pred. No. 0.0013;
24; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        29011292 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEBEAU B., MOREAU J., JACQUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DUBOIS S., MOREAU J.F., BATAILLE
ALPHA-CHAIN.
                                                                                        1093
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                                                                                                                                                                                                                                                                                                                                                         Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                          Length 422;
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                                                                      Query Match
Best Local :
                                                         Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-chain gene and its expression during pregnancy. EMBL; D86345; BNAD5907.1; -. PFAM; PF00041; fn3; 4. SEQUENCE 1093 as.
                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                     Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                 Submitted (JAN-1998)
                                                                                                                                                                                                                                                "Long and short forms of the ovine prolactin receptor: cDNA cloning and genomic analysis reveal that the two forms arise by different alternative splicing mechanisms in ruminants and in rodents.";
J. Mol. Endocrinol. 19:109-120(1997).
                                                                                                                                                                                                                                                                                                            BIGNON C., BINART N.,
DJIANE J.;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TIEMBLIER) 06,
01-JUN-1998 (TIEMBLIER) 06,
01-MAY-1999 (TIEMBLIER) 10,
PROLACTIN RECEPTOR LONG FORM
                                                                                                                                                                           PFAM; PF00041; fn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                046561
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 98001468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-WISTER-IMAMICHI; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                     Local
                                                                                                                                                                                                                             EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 IPVS-ENSGSNVIFSTVDD--VYGTVVFAGYPPDVPQKLSCETHDLKEIICSWNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 DKVVLAGSNMTICCISTTKVLSGQIGNTFRPLIHLYG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 98007878
      20
                               76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 LNGSRQQSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DPTILLIGSSLQATC----SIHGDTPGATAEGLYWTFNGRRLPSELSRLLNTSTLALALAN 56
                         SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYK 128
SILNGQS-----PPEKPKLIKCRSPGKETFTCWWEPGADGG--LPTNYTLTYR
                                                                    Similarity
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                                                                                                                       581 AA;
                                                                                                                                                                                      (JAN-1998) to t
(257; AAB96795.
                                                                                                                                                                                                                DJIANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                   24 1
581 1
; 65235 MW;
                                                                  9.98;
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                                                                                                                                                                                                                                                                                                                    ORMANDY C.,
                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                            06, Created)
06, Last sequence update)
10, Last annotation updat
FORM PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                     Score 99.5; r
Pred. No. 0.01
4; Mismatches
                                                                                                                   POTENTIAL.
PROLACTIN R
6792A7C7
                                                                                                                                                                                               EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 107.5;
Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                   SCHULER L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            581
                                                                                                                    RECEPTOR LONG FORM
7 CRC32;
                                                                 .014;
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                                                     18;
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                                                                                                                                                                                                                                                                                                                   KELLY P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAMURA T., SASAI
                                                                            Length
                                                     Indels
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Rattus.
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  65
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                                                  Gaps
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RESULT

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O18880
AC O18880;
DT O1-JAN-
DC EURARYO
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OC EURARY
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RX MEDLINE
RA SCHULER
RT *PIOLAC
RT tissues
RI EMBL;
DR PFAM; P
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Q64385
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Best Local S
Matches 29
                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                       Q16354 PRELIMINARY; PRT; 206 AA. Q16354; O1-NOV-1996 (TrembLrel. 01, Created) O1-NOV-1996 (TrembLrel. 01, Last sequence update) O1-NOV-1998 (TrembLrel. 08, Last annotation update) PROLACTIN RECEPTOR (FRAGMENT).
064385
                                                                                                                                                                                                                                                                        FUH G., WELLS J.A.; "Prolactin receptor antagonists that inhibit cancer cell lines.";
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endocrinology 138:3187-3194(1997).

EMBL; AF027403 AAB83999.1; -

PFAM; PF00041; fn3; 2.

SEQUENCE 296 AA; 33854 MW; 8B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-NOV-1998 (TrEMBLrel. 08, Last annotation
                                                                                                                                                                                                                                                                                                               ÆDLINE;
                                                                                                                                                                                                                                                                                                                                                         Sutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Sim
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                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prolactin receptor
                                                                                                             87
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                                                                                              LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKY 127
                                                                             LPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTY 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRILNTSTLALANINGSROOSGDNLVCHARDGSILAGSCLYVGLPPEKPFNISCWSRN 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRVVFILLLFLSVSLLNG--
                                                                                                                                                                                                                                PF00041;
                                                                                                                                                                                                                                             ol. Chem. 270:13133-13137(1995).
S78505; AAB34470.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 33.7
29; Conservative
                                                                                                                                                                                                                                                                                                               95286597
                                                                                                                                                                                                                                                                                                                                                                    Metazoa;
                PRELIMINARY;
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                       A.
                                                                                                                                                                                                                                fn3;
                                                                                                                                                                                                                                                                                                                                                     Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                      23950
                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.J., GAO J.,
heterogeneity
                                                                                                                                                9.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33854 MW; 8B40CCD8 CRC32;
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                                                                                                                                 Score 95; DB
Pred. No. 0.01
1; Mismatches
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Pred. No.
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8
              PRT;
                                                                                                                                                                                                      D7E57266 CRC32;
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in bovine feta
              432
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                                                                                                                                               DB 4;
0.012;
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                                                                                                                                                                                                                                                                                   the
                                                                                                                                    17;
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                                                                                                                                                           Length 206;
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                                                                                                                                                                                                                                                                                  growth
                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
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                                                                                                                                                                                                                                                                                  breast
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                                                                                                                               Gaps
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49

21 PGATA-EGLYWTFNGRRLPSELSRLLN--TSTLA--LALANLNGSROOSGDNLVCHARDG 75

SRLLQGPDSGLGHRLVLAQVDSPDE---GTYVCQTLDG 99

Query Match Best Local Matches

Similarity

9.3%;

Conservative

19;

Score 93.5; I Pred. No. 0.04 .9; Mismatches

.042;

11; 63,

Length

19;

Gaps

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20202525200000
 CARBOHYD
CARBOHYD
SEQUENCE
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EMBL; U14412; AAA
EMBL; X94162; CAA
EMBL; X94163; CAA
MGD; MGI:107426;
                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BALB/C, AND C57BL/6; TISSUE-EMBRYO; NEUHAUS H., BETTENHAUSEN B., BILINSKI P., GUENET J.L., GOSSLER A.; Dev. Biol. 166:521-542(1994).
                                                    DOMAIN
                                                                                     TRANSMEM
                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. J. 320:359-363(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HILTON D.J., HILTON A.A., RAICEVIC A., RAKAR S., HARRISON-SMITH GOUGH N.M., BEGLEY C.G., METCALF D., NICOLA N.A., WILLSON T.A.; "Cloning of a murine IL-11 receptor alpha-chain; requirement for gpl30 for high affinity binding and signal transduction.";
                                                                     DOMAIN
                                                                                                                       HAIN
                                                                                                                                                                                                                                                                              -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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STRAIN-C57BL/6 X CBA;
MEDLINE; 95045367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                     FAM; PF00047; 1g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   nouse genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1 PRECURSOR (NR1) (ETL2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Two differentially expressed interleukin-11 receptor genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILINSKI P., HALL M.A.,
                                                                                                                                                                                                                                                                                                                                                  :- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
:- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L11RA1 OR IL11RA OR ETL2 OR
                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: WIDELY EXPRESSED.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                  BINDS TO IL-11 WITH LOW AFFINITY,
                                                                                                                                                                                                                                                                                                      AINS ONE IG-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 05, Creat
(TrEMBLrel. 05, Last
(TrEMBLrel. 08, Last
                                                                                                                                                                             126; IL11RA1.
; fn3; 2.
                                                                                                                                                                                                                                                 CAA52908.1;
AAA53248.1;
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                                                                                                                                                                                                               CAA63873
                                                                                                                                                                                                                                  CAA63873.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND C57BL/6;
     46655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sciurognath1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-LIVER
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                                                                                                                                                Glycoprotein;
   Œ,
                                                                                                                                                                                                                  JOINED
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F65B3060 CRC32;
                                               CYTOPLASMIC (POTENTIAL) IG-LIKE C2-TYPE DOMAIN.
                                   POTENTIAL.
                                                                                               INTERLEUKIN-11 RECEPTOR ALPHA EXTRACELLULAR (POTENTIAL).
                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ET12/IL11
                                                                                                                                   OTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                ALPHA AND A BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H., GISSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence update)
annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                   BUT
                                                                                                                                              Immunoglobulin fold; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                NOT-TRANSDUCE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEATH J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
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136 XHMXGVPHCEPSLMPYPQGP 155

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                                                            TRANSMEM
DOMAIN
                                                                                                                                                                                                                      EMBL; U69491; AA
MGD; MGI:109123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1997 (TIEMBLTel. 02, Created)
01-FEB-1997 (TIEMBLTel. 02, Last sequence update)
01-NOV-1998 (TIEMBLTEL. 08, Last annotation update)
INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2 PRECURSOR (IL.
(IL-11RBETA) (INTERLEUKIN-11 RECEPTOR BETA CHAIN).
                                                                                                                                                                                      PFAM; PF00041; fn3; PFAM; PF00047; ig;
                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nouse genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BILINSKI P., HALL M.A., NEUHAUS H., GISSEL C., HEATH J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOBB L., HILTON D.J., WILLSON T.A., BEGLEY C. Structural analysis of the gene encoding the eceptor alpha-chain and a related locus."; Biol. Chem. 271:13754-13761(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CD-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
Eukaryota; Metazoa; (
Eutheria; Rodentia; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lpha-chain gene (IL11Ra2) with a restricted enomics 40:387-394(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOBB L., HILTON D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Two differentially expressed interleukin-11 receptor genes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 97129000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLINE; 97230451.

BB L., HILTON D.J., BROOK-CARTER P.T., BEGLEY C.G.;

dentification of a second murine interleukin-11 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lochem. J. 320:359-363(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 ESORESPSTGP--WPCPQDP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAIN-CD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    )225; 009074;
FEB-1997 (T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1RA2 OR IL-11RBETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                 CONTAINS ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIF
                                                                                                                                                                                                                                                                                  X94158; CAA63872.1; JOINED.
X94159; CAA63872.1; JOINED.
X94160; CAA63872.1; JOINED.
X94161; CAA63872.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-1; TISSUE=TESTIS;
97230451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .; TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                         BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                 IG-LIKE DOMAIN
432
367
393
432
102
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Mammalia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                        1RA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WIDELY EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                     TO THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                    Glycoprotein; Immunoglobulin fold; Signal.
                              CYTOPLASMIC (POTENTIAL)
IG-LIKE C2-TYPE DOMAIN.
                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                           INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the murine interleukin-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
ເຄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IL11RA2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 39
                                                                                                                                                                                                                                  EMBL; DL0144; ULC. PIR; JL0144; ULC. MGD; MGI:105304; 7 P00041; fr
                                  DOMAIN
DISULFID
CARBOHYD
CARBOHYD
                                                                                               DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                             PFAM; PF0004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TIEMBLIE1 01, Created)
01-NOV-1996 (TIEMBLIE1 01, Last sequence update)
01-NOV-1998 (TIEMBLIE1 08, Last annotation update)
INTERLEUKIN 6 RECEPTOR, ALPHA PRECURSOR
(MUTANT INTERLEUKIN-6 RECEPTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          000343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus. musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                               olasmacytomagenesis.";
J. Exp. Med. 171:2001-2009(1990).
-1- THIS PROTEIN IS A ABNORMAL INTERLEUKIN-6 RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BALB
                                                                                                                                                                                                                                                                                                                                                                                                                           Functional murine interleukin 6 receptor with the intracisternal A varticle gene product at its cytoplasmic domain. Its possible role j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 90278354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEGRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 ESQRESPSTGP--WPCPQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 XHMXGVPHCEPSLMPYPQGP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 VSGGMVTLKLGFPPARP-EVSCQAVDYENFSCTWSPGQ--VSGLPTRYLTSYRKKTLPGA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 PGATA-EGLYWTFNGRRLPSELSRLLN--TSTLA--LALANLNGSRQQSGDNLVCHARDG
                                                                                                                                                                                                                                                                                                               IN THE CDNA ENCODING THE ABNORMAL INTERLEUKIN-6 RECEPTOR THE REGION CORRESPONDING TO ITS INTRACYTOPLASMIC DOMAIN WAS REPLIVED A LONG TERMINAL REPEAT OF THE INTRACISTERNAL A PARTICLE (IAP) GENE, A MEMBER OF THE ENDOGENOUS PRORESPROVIRAL-LIKE
                                                                                                                                                                                                                                                                                                     ELEMENTS PRESENT IN THE GENOME OF MUS MUSCULUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSLKYKLRLVRSE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGVSAGTPVSWFRDGD-----SRLLQGPDSGLGHRLVLAQVDSPDE---GTYVCQTLDG 99
                                                                                                                                                                                                                                                                                          X51976; CAA36238.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 27.9
39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200
384
432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOTSUKA T., SAITO M., YAMASAKI K., TAGA T., HIRANO
                                                                                                                                                                                                                                                                        JL0144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                               fn3;
                                                                                                                                                                                                                                                       IL6RA.
    150
47901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.3%;
                                                                                                                                                                                                    Glycoprotein; Immunoglobulin fold; Signal.
   M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174
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₩.
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                               POTENTIAL.
POTENTIAL.
POTENTIAL.
EB5E7B93 CRC32;
                                                                                                                            EXTRACELLULAR IG-RELATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 93.5;
Pred. No. 0.
                                                              POTENTIAL.
                                                                              INTRACELLULAR
                                                                                                                                                          INTERLEUKIN-6
                                                                                                                                                                         MUTANT INTERLEUKIN-6 RECEPTOR.
                                                                                             IAP PORTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
⊗ ⊳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> P (IN CAA63872)
-> L (IN CAA63872)
C4FD7DEC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .042;
                                                                                                                                        RECEPTOR PORTION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                 IN WAS REPLACED
A PARTICLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               'n
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.2%; Score 92.5; DB 4; Best Local Similarity 33.9%; Pred. No. 0.14; Matches 21; Conservative 10; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                       01.NOV-1996 (TIEMBLIEL 01, Created)
01.NOV-1996 (TIEMBLIEL 01, Last seq
01.MAY-1999 (TIEMBLIEL 10, Last and
PROTEIN TYROSINE KINASE
                                                                                    MGD; MGI:10
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q62121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U60805; AAC50946.1; -. PFAM; PF00041; fn3; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MOSLEY B., DE IMUS C., FRIEND D., BOIANI N., THOMA B.,

COSMAN D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TIEMBLIE1. 03, Created)
01-MAY-1997 (TIEMBLE1. 03, Last sequence update)
01-MOV-1998 (TIEMBLE1. 08, Last annotation update)
0NCOSTATIN-M SPECIFIC RECEPTOR BETA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299650
                                                                                                                                                    ort, a mouse gene encoding a novel receptor-type protein-tyrosine inase, is preferentially expressed in the brain.";
                                                                                                                                                                                                                     EDLINE; 94150990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 PG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 PG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 NLNSVPFIRNKGTNIYCEASQGNVSEGMKGIVLFVSKVLEEPKDFSCETEDFKTLHCTWD 258
                                                                                                                                                                                                                                                          QUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 NLNGSR--QQSGDNLYCHARDGSI---LAGSCLYVGLPPEKPENISCWSRNMKDLTCRWT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 SRQQSGDNLYCHARDGSILAGSC-LYYGLPPEKPFNISCWSRN-MKDLTCRWTPGA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAN D.;
Biol. Chem. 271:32635-32643(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 TLLIGSSLQATCSIHGDTPGATAEG---LYWTFNGRRLPSELSRLLNTSTLALALANLNG 59
                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S--DTGDYL-CSLNDH--LVGTVPLLVDVPPEEP-KLSCFRKNPLVNAICEWRPSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSLPGATVTLIC-----PGKEAAGNVTIHWVYSGSQ-----NREWTTTGNTLVLRDVQL 84
PS00107; PROTEIN_KINASE_ATP; 1. PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Mammalia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110508 MW; 965DE8BC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          856 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          979 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARK L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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	SQ	SEQUENCE 856 AA; 93930 MW; 2DFBFC84 CRC32;
	p Q	Query Match 9.1%; Score 91.5; DB 11; Length 856;
	ма	Matches 48; Conservative 24; Mismatches 62; Indels 75; Gaps
	Qy .	11 QATCSIHGDTPGATAEGLYWTFNGRRLPSELSRLLNTSTLALALANLNGSRQQSGDNLVC 70
	D _b	143 QLSCEAVGPPEPVTIYW-WRGLIKVGGPAPFPFVL-NVIGVTQRIEFSC 189
**	δδ	71 HARDGSILAGSCLYVGLPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLH 121
	ğ	190 EARNIKGLATSRPAIVRLQAPPAAPFNTTVTTISSYNASVAWVPGADGLALLHSCTVQVA 249
	Q	121TNYSLKYKLRLVRSEXHMXGVPHCEPSLMPYP 152
	. 문	250 HAPGEWEALAVVVPVPPFTCLLRNLAPATNYSLRVRCANAL 291
	γO	153 QGPGPLHSLXDLGGSHQSPRLSKIXCP 179
•	<u>B</u>	Db 291 -GPSPTRIGALDNCGSAARILRISMB 316

11;

completed: September 16, 1999, 20:40:11 sec

GDN

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Pred. No. is the number of results score greater than or equal to the and is derived by analysis of the
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Match
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   32334
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(without alignments)
11.086 Million cell updates/sec
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Mouse melanocyte s
Mouse melanocortin
Sugar beet beta-1,
Mouse multidrug re
Sheep erythropolet
N-terminal of 48 k
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ORF 8 gene product
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G-protein coupled
G-protein coupled
Protein encoded by
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Bovine butyrophili
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                  al nervous cellulase
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Best Local s
Matches 30
                                                                                  Nicola
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                                                                                                                                                                                                                              Mus sp.
W09704091-A1.
                                                                                                      (AMRA-) AMRAD
                                                                                                                                                                                                                                                                                                                                                                           W10638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-1991
                                                                                                                                                                                               )6-FEB-1997.
.9-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                     23-JUN-1997
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Result No.

Score

Title: Perfect score:

Run

OM protein 9 :

Copyright

GenCore (c) 1993

- 1998

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Ltd.

Scoring table: Sequence:

> 45 39 28.1 164 بر بر W30082 W38705 Rat persephin. S. pneumoniae p pneumoniae phos

ALIGNMENTS

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Claim 5; Fig 1; 64pp; English.

The CDNA is derived from messenger RNA isolated from a mouse T-cell line after activation with concanavalin A. The cDNA was cloned by incorporation into a plasmid vector, which then transformed into E.coli. The plasmid vector also contained DNA segments from the SV40 virus, permitting expression of the CDNA after transfection into a mammalian host cell, such as monkey COS-7 cells. The polypeptide includes a potential leader sequence of about 19 AAs.
                 WPI; 97-132632/12.

Nucleic acid mol. encoding ligand for treatment of pref. neuronal, proliferation and differentiation
                                                                                                                                                                                                                                                                         Murine II-3 signal sequence.

LERK; ligand for eph-related kinase; receptor protein tyrosine kinase; cei cell differentiation; cell survival; cell-3; signal peptide; protein secret:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SCHE ) SCHERING CORP
(DNAX ) DNAX RES INST MOLEC.
(DNAX ) Lee FD, Rennick DM,
WPI, 85-100349/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence encoded by cDNA clone exhibiting multi-lineage growth factor activity.

Growth factor; multi-lineage; mast cell; haematopoietic.
                                                                                                                                                                                                                                                                                                                                                                                                       W10638 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New poly:peptide(s) having growth by recombinant DNA procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.
illarity 100.
Conservative
                                                                                                                            AU-004263
AU-006847
AU-007299
AU-007890
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US-539050.
US-590867.
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                                                                                                            OPERATIONS
71pp; English
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                                                                                                                                                                                                                                                                               secretion.
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Pred. No. 7.2e-14;
Mismatches 0;
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                                                                                                                                                                                                                                                                             cell porte
                                for eph-related kinase - us
cells to increase survival,
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                                                                                                                                                                                                                                                                                                             proliferation;
                                                                                                                                                                                                                                                                                              cell;
                                                                                                                                                                                                                                                                                              interleukin-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 166;
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PN W09/1200.

PD 01-MAX-1997.

PD 01-MAX-1996; AU0668.

PF 23-CCT-1996; AU-005135.

PR 23-DEC-1995; AU-007276.

PR 09-SEP-1996; AU-002208.

PA (AMRA-) AWRAD OPERATIONS PTY LTD.

PI Hilton DJ, Metcalf D, Nicola NA, Willson T, Zhang JG;

WPI; 97-250018/23.

PT Interleukin-13 useful to treat asthma, allergy or condition

PT exacerbated by 19E production

PS Example 2; Page 56; 93pp; English.

CC Using PCR, a derivative of novel haemoprotein receptor NR4 cDNA was

generated which encoded the interleukin-3 signal peptide (W09823)

and an N-terminal FLAG epitope tag (W09824) preceding the mature

1 The Thra7-Pro424) of murine NR4 (see also W09821). The
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RESULT
W56260
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W5
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Matches 30
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Best Local S
Matches 30
                                                                                                                                     Homo sapiens.
WO9810638-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A peptide sequence (W10638) comprises the signal sequence of mouse interleukin-3 (IL-3). Mammalian expression vector per-BOS was engineered to contain DNA for the IL-3 signal sequence and for a FLAG epitope. PCR fragments (see also T60970-72) coding for mature or soluble NLERK2 (see also W10637), a novel ligand for eph kinase (LERK), were cloned into the vector to allow prodn. of sequence 30 AA;
                                     27-FEB-1997;
                                                                                                                                                                                                                                          Therapeutic:
                                                                                                                                                                                                                                                                                      Construct
                                                                                                                                                                                                                                                                                                             16-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                       V56260 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 100.
30; Conservative
                                                                                                                                                                                                                                          containing mature interleukin-13 ic; IL-3 mediated condition; alle
                                                                                                                                                                                                        disease;
                                                                                                                                                                                                                                                                                                                (first entry)
AU-005374.
AU-002262.
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                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                     antibody; immunot
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Pred. No. 1e-
); Mismatches
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Pred. No. le-14;
Mismatches 0
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No. 1e-14;
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                                                                                                                                                                                                                               allergy; asthma;
                                                                                                                                                                                                                                                                           binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ļ.
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30

Query Match Best Local S Matches 30

Similarity

100.0%;

Score 139; DB 1 Pred. No. 1e-14; ; Mismatches

جاء :

Length

0

0

Conservative

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RESULT
W55017
PI Zhang J; MACUE M; MACHE M; MAKAF S; WillSon T;

PI Zhang J;

PM WPI; 98-260990/23.

PM New isolated haemopoietin receptor - used for developing products

PM New isolated haemopoietin receptor - used for developing products

PM of modulating proliferation, differentiation and survival of cells,

PM e.g. neuronal cells

Claim 29(1); Page 54; 182pp; English.

CC The mouse IL3 signal sequence was used to study the expression of mouse

CR R6.1. NR6.1 is a form of NR6 a novel Haemopoietin receptor (HR).

CC Interaction between the novel HR and a ligand facilitates proliferation,

CC differentiation and survival of a wide variety of cells. The HR and it's

CC derivatives can be used for modulating the activity of the receptors e.g.

CC different cells and tissues in vitro and in vivo. They can be present in

CC and survival. The products can also be used for detection and diagnosis,

CC e.g. for cancers or predisposition to cancers, or for drug screening.

SO Sequence 30 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 30
                                                                                                                                                                                                                                                                                      19-MAR-1998.
11-SEP-1997; G02479.
11-SEP-1996; AU-002246.
11-SEP-1996; AU-002246.
11-SEP-1996; AU-002246.
                                                                                                                                                                                                                                                                                                                                                                                                                    Murine II3 signal sequence
Haemopoletin receptor; cell
cell survival; therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated interleukin-13 binding protein - used to develop products for therapy e.g. for allergic conditions such as asthma or for diagnosis or detection

Example 14; Page 52-53; 69pp; English.

The II-13 binding protein and related therapeutic molecules can be used in the antagonism of at least one II-13 activity. They can be used for treating II-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered II-13 after II-13 after II-13 after II-13 conditions of the products can also be used as diagnostic agents, e.g. for immunotherapy and may also be used as a diagnostic tool.

Sequence 359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMRA-) ALL
                                                                                                                                                                                                                                                            Alexander W, Fabri
Kojima T, Maeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W55017
W55017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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ilarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   therapeutic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                           Farley A, Hilton
sh A, Nicola NA, F
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Pred. No. 1
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.7e-13;
s 0;
                                                                                                                                                                                                                                                            Kikuchi Y,
r S, Willson
                                                                                                                                                                                                                                                                                                                                                                                                                              differentiation;
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                                                                                                                                                                                                                                                                                                                                                                                                                screening;
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RESULT
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Best Local Similarity
""+"hes 9; Conserv
 Anther
Anther
                                                       R71911;
                                  22-NOV-1995 (first entry)
                                                                     R71911 standard;
                                                                                                                                                                                                                                                                                                                     treatment of
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                      receptors can be used in a novel, claimed method of screening for compounds which modulate the binding of a Wnt polypeptide (secreted proteins involved in cell-to-cell signalling) to a Wnt receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This protein comprises the Drosophila frizzled-2 protein encoded the Drz2 gene (see 189885). It is a receptor for wingless (Wg), acting as a signal transducing molecule, and is an example of a receptor (WntR). Other novel frizzled family members have been identified in human, mouse and Caenorhabditis elegans (see w31268-74) and are considered also to be Wnt receptors. Wnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc_difference
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(SYRD ) UNIV LELAND STANFORD JUNIOR.
ANDRIEW D. Bhanot P, Brink M, Hsieh J
Nusse R, Samos CH, Wangy;
MPI; 97-526631/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-1997.
11-APR-1997; U06049.
12-APR-1996; US-015307.
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                                                                                                                                                                                                                                                                                                                                                        growth, development and produlators identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila frizzled-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W31267 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-1998
                                                                                                                                                              383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dentification of Wnt receptor binding modulators - useful for reatment of cancer and growth, development or proliferation related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -PSDB; T89885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aim 2; Page 23-25; 61pp;
                                                                                                                                                                                             1 MVLASSTTSIHTMLLLLLMLFHLGLQASI 29
                                                                                                                                                                                                                                                                                                                                                                                       is involved in (mammary)
                                                                                                                                                          LLLRESSTGPHSCTLVFLLTYFFGMASSI 411
 specific p
                                                                                                                                                                                                                                                                                                                                       diseases related
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brosophila frizzled-2 protein;
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671
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269
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                                                                    Protein;
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                                                                                                                                                                                                                                                 34.5%;
Brassica napus; antisense
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deletion of
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                                                                                                                                                                                                                                                                                                                                     the claimed method are useful lated to these conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                           Score 48; DB Pred. No. 16; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     cancer and other processes involving
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                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                               Length 694
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Best Local
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(MYCO ) MYCOGEN CORP.
Narva KE, Schnepf HE,
WPI; 98-086971/08.
                                08-JAN-1998.
01-JUL-1997; U11658.
01-JUL-1996; US-674002.
                                                                                                                                                                       Misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus thuringiensis toxin designated 85; Toxin; lepidopteran pest; control; Agrotis Heliothis virescens; Helioverpa zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is encoded by an anther specific gene derive Brassica napus. This gene may be expressed as antisense is Cruciferae plant causing pollen formation to be modified esp. useful in the production of male sterile plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A gene expressed specifically in anther(s) - preparation of male sterile Cruciferae plants Claim 1; Page 5; 6pp; Japanese.
                                                                  WO9800546-A2.
                                                                                                                                                                                                                                           Misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus thuringiensis.
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(MITU ) MITSUBISHI KASEI
WPI; 95-135897/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46836 standard; Protein;
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l Similarity 38.5%;
10; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                     /note=
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                                                                           /label= unknown/
/note= "encoded
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/note= "encoded
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/note encoded
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        Stockhoff BA,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                           ipsilon; black cutworm;
         Wicker
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determining HAPO167 protein levels. HAPO167 proteins can be used to screen for agonists and antagonists which bind to the protein. These can be used in treatment to activate (agonist) or inhibit (antagonist) can be used in treatment to activate (agonist) or inhibit (antagonist) can be used in treatment to activate (agonist) or inhibit (antagonist) can be used in treatment to direct administration of antisense conditions associated with a lack of HAPO167 protein. Gene therapy may also be used to affect endogenous HAPO167 protein production. HAPO167 antibodies are useful for inducing an immune response to immunise and correct against diseases, and for isolating HAPO167 clones or purifying the protein by affinity chromatography. HAPO167 proteins can be administered directly or as a vaccine to inoculate against disease. CC Diseases diagnosed, prevented or treated include: infections caused by Enseases diagnosed, prevented or treated include: infections caused by HIV-1 or -2; pain; cancer; bulinia; asthma; parkinson's disease; acute casteoporosis; angina pectoris; myocardial infarction; ulcers; allergies; benign prostatic hypertrophy; and psychotic and neurological disorders; including delixium, anxiety, schizophrenia, manic depression, dementia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a G-protein coupled receptor (HAPO167) protein. HAPO167 proteins and polynucleotides are useful for diagnosing susceptibility to diseases by detecting mutations in the HAPO167 gene, and can diagnose diseases associated with HAPO167 imbalance by determining HAPO167 protein levels. HAPO167 proteins can be used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences.
Sequence
including delirium, any severe mental retardati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 23-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New G-protein coupled receptor HAPO167 polypeptide and polynucleotide - useful as diagnostic reagents and for and treatment of cancer, HIV_infections and osteoporosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; X03844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-1998; 303521.
23-OCT-1997; US-956322.
11-JUN-1997; US-049329.
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Claim 2; Page 56; 183pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP. Mao JY, Sathe GM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W30637 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      luman 7-transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uman; HAPO167; 7-transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
tes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 HTMLLLLMLFHLGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLAIPILVILFHLGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypertension; urinary retention; osteoporosis; na pectoris; myocardial infarction; psychotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypertrophy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor
      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                652 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkinson's disease; acute heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAPO167 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor; infection; ba
pain; cancer; bulimia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 9;
8d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lepidopteran
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   Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  obtain
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253 IQNTSTSLHLQLSLCLFLAHL

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23

Query Match
Best Local Similarity
Matches 9; Conserv

Conservative

5

Mismatches

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Gaps

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32.4%;

Score 45; Pred. No.

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                                            protein. HAPO167 proteins and polynucleotides are useful for diagnosing cand can diagnose diseases by detecting mutations in the HAPO167 gene, and can diagnose diseases associated with HAPO167 imbalance by determining HAPO167 protein levels. HAPO167 proteins can be used to screen for agonists and antagonists which bind to the protein. These can be used in treatment to activate (agonist) or inhibit (antagonist) can be used to response to prevent expression, or HAPO167 protein. Gene therapy may called the sequences to prevent expression, or HAPO167 protein. Gene therapy may called be used to affect endogenous HAPO167 protein. Gene therapy may called be used to affect endogenous HAPO167 protein. Gene therapy may called be used to affect endogenous HAPO167 protein. Gene therapy may called be used to affect endogenous HAPO167 protein. Gene therapy may called be used to affect endogenous HAPO167 protein production. HAPO167 called and protein by affinity chromatography. HAPO167 clones or purifying the protect against disease, and for isolating HAPO167 clones or purifying chamiltered directly or as a vaccine to inculate against disease. Diseases diagnosed, prevented or treated include: infections caused by HAPO167 callude: hypotension; bypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcers; allergies; benign prostatic hypertrophy; and psychotic and neurological disorders, including delirium, anxiety, schizophrenia, manic depression, dementia, severe mental retardation and dyskinacias, manic depression, dementia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                severe mental retardation a or Gilles de la Tourette's
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New G-protein coupled receptor HAPO167 polypeptide and polynucleotide - useful as diagnostic reagents and for and treatment of cancer, HIV infections and osteoporosi Disclosure; Page 13; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein coupled receptor; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; ulcer; allergy; angina pectoris; myocardial infarction; psychotic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is protein. HAPO167 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; HAPO167; 7-transmembrane receptor; infection; ba fungal; protozoan; HIV-1; HIV-2; pain; cancer; bulimia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 99-047874/05.
N-PSDB; X03845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP.
MAO JY, Sathe GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1997; US-956322
11-JUN-1997; US-049329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prostatic hypertrophy;
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9; Conserv
521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           652 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7-transmembrane receptor HAPO167 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a partial G-protein
                                     and dyskinesias,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404
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43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection; bacterial;
                                   such as Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prevention
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Matches
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Best Local
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10-JUL-1996; US-678200.
09-APR-1996; US-015167.
05-JUN-1996; WO-U09286.
06-JUN-1996; US-019202.
      DNA, ligands, antibodies, etc Claim 1; Page 42-44; 65pp; English.

This sequence represents a human G-protein coupled receptor of the invention. The protein or cells expressing the DNA encoding it can be used to screen for agonists or antagonists of the receptor, which can be used as drugs for treating various diseases (none disclosed). The DNA can also be used for practice drug design based on comparisons with extructurally analogous ligands and receptors. DNA encoding the protein can be used for gene therapy for diseases caused by a deficiency of the receptor. The DNA can also be used to detect abnormalities in the gene encoding the receptor. The protein or fragment can be used to determine levels of receptor ligands in vivo. The antibody can be used in assays to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Breast cancer genes - used to develop products to design or screen diagnostic reagents or therapeutic compounds Claim 17; Fig 24; 118pp; English.

W58774-W58804 are translated protein fragments from the novel human breast cancer gene, CH9-2all-2 isolated from a 3.5 kb DNA fragment. This fragment can be used for identifying genes and gene products that are intimately related to malignant transformation or maintenance of the malignant properties of cancer cells. It can also be used to design or screen diagnostic reagents or therapeutic compounds. Kits are included within the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen L, Smith H; WPI; 97-512705/47.
                                                                                                                                                                                                                                                    Fukusumi S, Hinuma S, Kawamata
                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
EP-845529-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 W55029 standard;
W55029;
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                                                                                                                                                                                                     New human G-protein coupled receptor protein -
                                                                                                                                                                                                                        WPI; 98-288746/26.
N-PSDB; V27174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapeutic; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1998
                                                                                                                                                                                                                                                                  27-OCT-1997; 308562.
29-OCT-1996; JP-286823.
(TAKE ) TAKEDA CHEM IND LTD.
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                                                                                                                                                                                                                                                                                                                                                               -protein coupled
-protein coupled
hort form; human.
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11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein; 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        scope of the invention.
1268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                              receptor, short receptor; gene 1
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; malignant transformation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB
Pred. No. 1.8e
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                            therapy;
                                                                                                                                                                                                                                                                                                                                                                                              form.
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1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                            abnormality detection;
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                                                                                                                                                                                                     and corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA, ligands, antibodies, etc.

Claim 2: Page 45-47; 65pp; English.

Chaim 2: Page 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
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Best Local
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                                                                                                                                                                                                                                         07-DEC-1998 (first entry) Protein encoded by ORF 266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fukusumi S, Hinuma S, Kawamata WPI; 98-288746/26. N-PSDB; V27175.
                                                                                                                                                                                                                        Multiple antibiotic resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W55030 standard; Protein;
                                                                                  28-AUG-1992;
                                                                                                  08-AUG-1994; 225480.
08-APR-1994; US-225480
                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                   bacterial resistance;
                                                                                                                                                                                                                                                                    07-DEC-1998
                                                                                                                                                                                                                                                                                                      W71460 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                         184 VTESSYSAYAIMLLALVVFAVGIVGNLS
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8; Conserv
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    Mismatches

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therapy; abnormality detection;
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Best Local Similarity 30.3
Matches 10; Conservative
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Best Local (
                                                                                                                                                                                                             and over expresses at least one gene coding for a protein that mediates cellular clearance of antibiotics or other substances that are toxic for the microorganism. A process is described for producing L-cysteine, in which intracellularly produced L-cysteine reacts with an intracellular ketone or aldehyde in a microorganisms to form a thiazolidine derivative. The thiazolidine derivative is secreted from the microorganism by means of a protein that mediates cellular clearance of antibiotics or other substances that are toxic for the microorganism, and optionally after separating the thiazolidine derivative. L-cysteine is recovered by equilibrium displacement of the reaction equilibrium between L-cysteine and the thiazolidine derivative in the direction of L-cysteine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 16-17; 33pp; German.

This sequence is a fragment of an antibiotic efflux protein from Escherichia coli strain K12 which is used an a method resulting in a novel microbial strain which is suitable for the fermentative production of L-cysteine, L-cystine, N-acetyl-serine and/or thiazolidine derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resistance (mar) operon. Antisen mar operon can be used to lower antibiotics.
Sequence 266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microbial strain over-expressing antibiotic efflux gene - for producing L-cysteine, L-cystine, N-acetyl-serine and/or thiazolidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents the protein encoded by open reading frame (ORF) 266 an Escherichia coli multiple antibiotic resistance (mar) operon. Antisense molecules directed against t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding activator of multiple antibiotic resistance op
and anti-sense molecule for lowering antibiotic resistance
bacteria
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2-MAY-1998; 109269.
9-JUN-1997; DE-026083
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intibiotic efflux gene; fermer
acetyl-serine; thiazolidine
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                                         1 MVLASSTTSIHTMLLL----LLMLFHLGLQASI 29
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LILDGSATMIHSLYTIDMTTILSLMYLAFVATI 233
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Pred. No.
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                                                                                          Mismatches
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                                                                                                          . 52;
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Search completed: September 17, 1999, 03:08:19 Job time: 310 sec

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Result
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Perfect score:
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/cgn2_6/ptodata/2/laa/ptous9_COMB.pep:*
/cgn2_6/ptodata/2/laa/backfiles1.pep:*
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Appl
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REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
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RESULT 5304637-4 ;Patent N ; Patent N		4444 01284 048
RESULT 1 5304637-4 ;Patent No. 5304637 ; APPLICANT: DOR		37 37 37 37 37 37 37 5
4637 DORSSER		27.3 27.3 27.0 27.0 27.0
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os c	>	PCT- US-00-SD US-00-SD
LT 1 637-4 ent No. 5304637 ent No. 5304637 APPLICANT: DORSSERS, LAMBERTUS C.J.; WAGEMAKER, GERARD; VOS.	ALIGNMENTS	PCT-US95-07294-2 PCT-US95-16144-3 US-07-745-206A-7 US-08-455-550-21 US-08-455-543A-45 US-08-223-305C-45
GERARD; VOS,		Sequence 2, Appli Sequence 3, Appli Sequence 7, Appli Sequence 21, Appli Sequence 45, Appli Sequence 45, Appli
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US-08-208-007A-13
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TITLE OF INVENTION: EX
INTERLEUKIN-3 AND MUTEINS
NUMBER OF SEQUENCES: 3
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Best Local Similarity
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            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: NO. 5:
APPLICATION UNMER: NO. 5:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                       SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/2
FILING DATE: March 8, 1994
                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          APPLICANT: HASTINGS, ET AL.
TITLE OF INVENTION: Human Osteoclast-Derived Cathepsin
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                               COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                                                                                                    COUNTRY: U. ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 249,184 FILING DATE: 16-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/494,182 FILING DATE: 13-MAR-1990
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                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION
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NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08208007A
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E: CECCHI, STEWART
6 BECKER FARM ROAD
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GREGORY D
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8, 1994
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Pred. No
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Best Local Similarity
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                                                                    Query Match
Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
NAME: GATES EDWARD R.
REGISTRATION NUMBER: 31,61
REFERENCE/DOCKET NUMBER: 7
                                                                                                                                                                                                  NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                       COLECULE TYPE:
                                                                                                                                                                                                                   TELEFAX: 617-720-3500
161 LILDGSATMIHSLVTIDMTTILSLMYLAFVATI 193
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/938,085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201-994-1744
FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             LENGTH: 266 amino acids
TYPE: amino acid
                       1 MVLASSTTSIHTMLLL----LLMLFHLGLQASI 29
                                                                                                                                                    POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 TMLLLLLMLFHLG 24
                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                               PUTER READABLE FORM:
EDIUM TYPE: Floppy disk
OMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                       ASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPONDENCE ADDRESS:
RESSEE: WOLF, GREENFIELD & SACKS, P.C.
EET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                ICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                         ARE: Patentin Release #1.0, Version #1.25 APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02210
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5817793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STUART B.
                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
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                                                   Score 42; DB
Pred. No. 30;
9; Mismatches
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Pred. No.
                                                               DB 2;
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                                                                            Length 266
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JS-08-466-906B-4
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Best Local (
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                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                           171 IVSSTLFITYYKHTAVLLCLVTFFLAMLA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                    RRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                     3 LASSITSI----HIMLLLLMLFHLGLQA 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: UFILING DATE: 19920410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: No. 5532347nan,
REGISTRATION NUMBER:
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                                                                                          DRESSEE:
                                                                                                                              LE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                  ECULE TYPE:
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                                                                                                                                                                                   INFORMATION:
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                           60606
                                                                Chicago
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                                                                           300 South Wacker Drive
                                                                                                                                                        Mount joy,
                                       USA
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                                                                                                                                                                      Cone, Roger D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA.
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SYSTEM: PC-DOS/MS-DOS
                                                                                      McDonnell Boehnen Hulbert & Berghoff
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                                                                                                                                                                                                                                                                                                                                                                                                               protein
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                                                                                                                                     Melanocyte Stimulating Hormone Receptor
                                                                                                                                and Uses
                                                                                                                                                          Kathleen G
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Pred. No. 50;
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Query Match
                                                          NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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 OLECULE TYPE:
                                                                                                                           TELEPHONE: (415) 677-7000
                                                                                                                                                                                                      TORNEY/AGENT INFORMATION:
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                                                                                                                                                                        NAME: GRACEY, NANCY J
REGISTRATION NUMBER:
                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/164,292B
FILING DATE: 09-DEC-1993
                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: F
SOFTWARE: PatentIn
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                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                      SOFTWARE:
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                                                                                                            ELEFAX:
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                                             ENGTH:
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                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                  345 California Street
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                                              308 amino acids
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                                                                                                            (415) 677-7522
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protein
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Pred. No.
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US-08-164-292B-18
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                                                                                                               OTHER INFORMATION:
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              OTHER INFORMATION:
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ENGTH: 22 amino acids
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                                                                                                                                           AME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                      ORNEY/AGENT INFORMATION
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                                                                     INFORMATION
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CA
                                                                                                                                                                                                                          amino acid
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1..22
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                                                                                                                                                                    porcine
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lilespie, William
                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                     August 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                          July 12, 1995
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/note= "putative signal-anchor
domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Release #1.0, Version #1.25
                                                                  /note- "amino terminal amino acid sequence of the porcine 48 KDa Gal Betal, 3 GalNAC alpha 2,3 sialyitransferase"
                                                                                                              'label=, 48KDa
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6:
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Pred. No.
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US-08-446-875-6

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LOCATION: 1.581;
OTHER INFORMATION:
JS-08-724-394A-3
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Best Local Similarity
7; Conserve
                                    Query Match
Best Local Similarity
                                                                                                                                                   TPE: amino acids
STRANDEDNESS: no+
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                       MPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
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SIHTMLLLLLMLFHLGLQASIS 30
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                                                                                                                                                                                                                                                                                         : Fitts, Renee F
STRATION NUMBER:
                                                                                                                                                                                                                                                                  MMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              RY: USA
94111-3834
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APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    San Francisco
                                                                                                                                                                                                                                                                                                                                              ATION NUMBER:
DATE: 01-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08724394A
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                                                                                                                  Region
1..581
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                                                                                                                                                                                                                                                                                                                                 01-OCT-1996
N: 536
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                                                                                                                                                                            not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   John N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.8%;
                                    28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Megabase Transcript Map: No. 5872237el Sequences and Antibodies Thereto
                                                                                                 /note- "BTF2"
                                                                                                                                                                                                                                                                                                                                                        US/08/724,394A
                                                                                                                                                                                                                                                                                          35,136
                                    Score 40;
Pred. No. 1
                                                                                                                                                                                                                                                                             017957-000100
                        Mismatches
                                            Length 581;
                      Indels
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Query Match
Best Local Similarity
---hes 9; Conserve
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INFORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                         ITLE OF INVENTION:
ITLE OF INVENTION:
                                                                                                                                                                                                                                                                          13 MLLLLMLFHLGL 25
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OPERATING SYSTEM: PC-DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: Herew
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                               DRESSEE:
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                                                                                                                  INFORMATION:
ANT: KINET, Jean-Pierre
Alexandria
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20005-3934
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                                                                                                                                                                  Application US/07869933
         1800 Diagonal Road, Suite 500
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Wen, Danyi
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Boston, MA 02115
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                                                                                  ISOLATION, CHARACTERIZATION, AND USE OF THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
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COMPUTER READABLE FORM:

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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 URRENT APPLICATION DATA:
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                           IOR APPLICATION DATA:
APPLICATION NUMBER: US 07/869,933
FILING DATE: 16-APR-1992
IOR APPLICATION DATA:
                                                                                                                           APPLICATION NUMBER: US/08/201,879A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFERENCE/DOCKET NUMBER:
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Similarity 39.3%;
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AMINO ACID
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FCRI beta subunit
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Pred. No. 6
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LING DATE: 19-AP:
PLICATION NUMBER:
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60 STATE STREET, SUITE 510
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                                                                                                                        DOCKET NUMBER
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protein
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Pred. No. 6
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   TITLE OF INVENTION:
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                                                                                                                                                                                                                                   Local Similarity
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PETWARE: ASCII text

RENT APPLICATION DATA:

PLICATION NUMBER: US.
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                                                INFORMATION:
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IUM TYPE: Floppy disk
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APPLICATION DATA:
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NG DATE: 19-APR-1991; 13-JAN-1993
                                                                                                                                                                                                                                                                                                                                        amino acid
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60 STATE STREET, SUITE 510
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        No. 5856165el Alkaline Cellulase and Methods of
Producing Same
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Pred. No.
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4; Mismatches
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Query Match
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Conservative
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application PC/TUS9501618 GENERAL INFORMATION:
                                                                      TELEFAX: (617) 227-59
NFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                           SEQUENCE CHARACTERISTICS LENGTH: 206 amino acid
                                                                                                      TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLE OF INVENTION:
                                                                                                                                     REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                ORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:| :||: | || :|
5 TTIFAVLLMTLALFSIG 21
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TYPE:
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Score 39; DB Pred. No. 61;

DB 3; Length 206;

Indels

Search completed: September 16, 1999, 20:41:12
Job time: 5441 sec

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd

OM protein - protein search, using sw model

Run on: September 16, 1999, 20:42:11; Search time 49.27 Seconds (without alignments)

Title: US-09-037-657-32 Perfect score: 139

1 MVLASSTTSIHTMLLLLLMLFHLGLQASIS 30

Scoring table: BLOSUM62

Sequence:

hed: 122810 seqs, 40065486 residues

Database : PIR_60:* 1: Pir1:* 2: Pir2:* 3: Pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2 JE0258 cytochro 2 JH0451 cytochro 2 S58996 NADH deh 2 A55405 adenylat 2 S16762 gonadorr 2 A60626 glycopro	
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	cytochrome P450 is cytochrome P450 2C NADH dehydrogenase adenylate cyclase gonadotropin alpha glycoprotein hormo
cytochro cytochro NADH deh adenylat gonadotr glycopro	cytochrome P450 is cytochrome P450 2C NADH dehydrogenase adenylate cyclase gonadotropin alpha glycoprotein hormo
	me P450 is me P450 2C ydrogenase e cyclase opin alpha tein hormo

Cross-references: GB.MZ0128; NID:g198384; PID:g387387 Comment: This glycoprotein, produced by bone marrow centiation of hematopoletic cells. Reference number: I53994; MUID:86083183 Accession: I53994 Title: Determination of the glycosylation patterns, disulfide linkages, and protein Reference number: A38860; MUID:93075774 Reference number: 1tle: Isolation and characterization of a genomic DDD mouse interleukin-3 gene. ross-references: GB:K03233; NID:g198338; PID:g387385 103-107, 1985 translated from GB/EMBL/DDBJ T.; Lee, F. l. Acad. Sci translated from GB/EMBL/DDBJ -166 <RES> -145,'A',147-166 <YOK> ; 69/3; 101/3; 115/3 interleukin-3 source: bonds were shown between Cys residues at 43 and either 106 or 105, fide bond 105-166 is not conserved in most orthologs NID:g199083; PID:g387421 Schreurs, J.; Deinzer, M.L. ; Arai for murine interleukin 3. a mouse cDNA clone that expresses mast-cel Arai, N.; Mosmann, cells, by mitogen or antigen-ac T.; Nabel, G.; Canto

Similarity

82.1%;

5.2e-06;

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                                             A; Molecule type: mRNA
A; Residues: 1-168 <ESA>
                                                                           A;Reference number: JC6566
A;Accession: JC6566
                                                                                                      Gene 211, 151-158, 1998
A;Title: Cloning, biological
                                                                                                                                       R; Esandi, M
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                                                                                                                                                                                                .nterleukin-3 beta protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Reywords: cytokine; glycoprotein; growth factor; F;1-26/Domain: signal sequence #status predicted <
                              ;Cross-references: GB:U81492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 30
Comment: This protein is a superfamily: interleukin-3
                                                                                                                                                                Date: 05-Dec-1998 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: interleukin-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reference number: S07369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Rattus
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                                                                                                                                     van Someren,
                                                                                                                                                                                                                                                                                                                                                                                                                                   site: carbohydrate (Asn)
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                                                                                                                                   G.D.; van der Velde,
            hematopoietic
                                                                                                        characterization
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Pred. No. 1.1e-11;
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            growth
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                                                                                                                                  I.; van Bekkum,
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            factor
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Query Match

69.1%;

Score

96;

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Length

168;

NID:g12879;

PID: g12881

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submitted to the EMBL
                                                                                                                                                            NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Crithidia oncopelti
C;Species: mitochondrion Crithidia oncopelti
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: flhA
C; Superfamily: regulatory protein
C; Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardin, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; May, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Porter Rieger, M.; Rivolta, C.; Rocha, E.; Scoftone, B.; Rose, M.; Sadale, Y.; Sato, T.; Scan, A.; Authors: Schielch, S.; Schroeter, R.; Scoffone, F.; Schiguchi, J.; Sckowska, A.; Sakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiy, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshica, A.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil A.; Reference number: A69580; MUID:98044033
                         A; Residues:
                                                                 A; Accession:
                                                                                        A; Reference number:
                                                                                                                                                          C; Accession:
                                                                                                                                       R; Maslov,
A/Cross-references: EMBL: X56015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Cross-references: EMBL:X63698; NID:g39916; PID:g39917
R;KUNSt, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.C.; Bron, S.; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Falkette, 390, 249-256, 1997
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Matches 13
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ritle: Bacillus subtilis Fhha: a flagellar protein related Recession: $33664; MUID:93225816

Molecula - 33664
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                  1-437 <MAS>
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S34958
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ce: strain 168
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Library, Oct
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                                                                                                         K.; Kolesníkov, A.A.
tober 1990
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V.;
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
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Best Local Similarity 34.4
Matches 11; Conservative
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:Title: Sequences of six genes and
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Residues: 1-443 <DEL>
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                                                                                         ecule type: DNA
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                                                                                                                                                                                                        s-references: EMBL:U65589
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brids: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Jul-1998
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                                                                                                                                                                                                                     1-694 <BHA>
transmembrane protein
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                                                                                                                                                                                                                                                       acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        precursor dfz2 - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                        la melanogaster
                                                 ",418-694 <BHW>
EMBL:U65589; NI
                                                                                                                                                                                                                                                                                                                                                 Harryman Samos, C.;
                                                                                                                                                                                                                                                                                                               the frizzled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.4%; Score 48.5;
34.4%; Pred. No. 22;
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                                                                                                                                                                                                                                                         not shown
                                                 NID: g1518050;
                                                                                                                                             July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                               from
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                                               PID:g1518051
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                                               밁
                                                                                                                      Matches
                                                                                                                                                        Query Match
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134 LALASSEGVIFSLILLALSIFH

5; 22

MVLASSITSIHTMLLLLLMLFH

Local Similarity

45.5%;

Score 47; DB Pred. No. 14;

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Length 160;

Mismatches

0;

Gaps

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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A;Reference number: A69250; MUID:98049343
A;Accession: B69318
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                                                                                                                                                                         A; Accession:
1;Gene: PH0566

    Ohfuku, Y.; Funahashi, T.; Tanaka, Y.; NUUUH, Y.; AUTONIA, A.S. 55-76, 1998
    AR Res. 5, 55-76, 1998
    Pittle: Complete sequence and gene organization of the genome of a hyper-thermophilise representation of the genome of a hyper-thermophilise representation of the genome of a hyper-thermophilise representation.

                                                                        Cross-references: GB:AP000002; NID:g3236129; PID:d1030598; PID:g325697
                                                                                                                                                                                                                                                                                  Kawarabayasi
                                                                                                                                                                                                                                                                                                                    Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Aug-1998
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                                      this accession
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                                                                                                                                              preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                          1-160 < KAW>
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9; Conser
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                                                                                                                                                                                                                                                       Funahashi, T.; Tanaka, T.; Kudoh, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                      cus horikoshij
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                                        replaces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.8%;
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                             an interim accession for a sequence replaced by GenBa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47; DB Pred. No. 20; 3; Mismatches
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Pred. No.
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37;
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Yamazaki,
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Kushida, l
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Kirkness, E
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Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Conton, M.D.; Spriggs, T.; Conton, M.D.; Woese, C.R.; Venter, J.C.
                                                                                                                                                      conserved hypothetical protein AF0094 - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Jun-1998
                                                                                                R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; K
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C;Species: Emer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       asein kinase, and one sequence that resembles a nuclear localization C; Comment: This protein is part of a regulatory pathway that includes ter mitosis and prevent them from leaving mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Engle, D.B.; Osmani, S.A.; Osmani, A.H.; Rosborough, S.; Xiang, X.; Morris, N.R. J. Biol. Chem. 265, 16132-16137, 1990
A;Title: A negative regulator of mitosis in Aspergillus is a putative membrane-spanning A;Reference number: A37879; MUID:90375468
A;Accession: A37879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: bimE protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title: Isolation and char. Reference number: S33612;
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                                                                                                                                                Accession: F69261
                                                                                                                                                                                                                                                                                                                                                                               Matches
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Cross-references: GB:M59705, GB:J05607, NID:g168026
Note: in addition to three predicted transmembrane
                                                                Fleischmann, R.D.; Quackenbush, Iodek, A.; Zhou, L.; Overbeek, Rture 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession:
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Emericella nidulans, Aspergillus nidulans
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          sequence of the
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Pred. No. 1.
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1.8e+02;
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                                            Artiach, P.;
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    sulfate-reducing archaed
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                                          Kaine, B.P.;
                                                                                McDonald,
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Query Match
Best Local S
Matches 10
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submitted to the EMBL Data Library, June 1993
A; Description: Inhibition of an in vivo antigen-specific IgE response
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A; Residues: 1-653 <SOR>
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J. Biol. Chem. 269, 6615-6621,
A;Title: Cloning of a Na/P-1 c
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A; Status: pre
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A; Residues: 1-342 <KLE>
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A;Accession: F69261
                                                                                                                                                                                                                                                            Residues: 1-309 <FLO>
Cross-references: EMBL:X73579; NID:g313672; PID:g313673
Superfamily: IgE receptor II; C-type lectin homology
Superfamily: IgE receptor tell; cross-control tell; cro
47-309/Domain: extracellular *status predicted <EXT>
126-309/Product: soluble IgE-binding factor (29K) *ss
149-309/Product: soluble IgE-binding factor (25-27K)
164-283/Domain: C-type lectin homology <LCH>
192-283,260-274/Disulfide bonds: *status predicted
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Scoring table: BLOSUM62

Searched: 77977 seqs, 28268293 residues

Database : SwissProt_37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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KNEPPER T.P., ARBOAST B., SCHREURS J., DEINZER M.L.;
"Determination of the glycosylation patterns, disulfide linkages, and protein heterogeneities of baculovirus-expressed mouse interleukin-3 by mass spectrometry.";
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"Molecular cloning of cDNA for murine interleukin-3.";
NATURE 307:233-237(1984).
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MEDLINE; 8525765.
MEDLINE; 8525765.
FUNG M.-C., YOUNG I.G.;
CANVEBELL H.D., YMER S., FUNG M.-C., YOUNG I.G.;
"Cloning and nucleotide sequence of the murine interleukin-3 gene.";
EUR. J. BIOCHEM. 150:297-304(1985).
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IIVATAKE S., YOKOTA T., LEE F., ARAI K.-I;

Structure of the chromosomal gene for murine interleukin

BROC NATE, ACAD. SCI. U.S.A. 82:316-320(1985).
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ROC. NATL. ACAD. SCI. U.S.A. 81:1070-1074(1984).
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NTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING ACTOR) (P-CELL STIMULATING FACTOR)
NTERLEUKIN-3 PRECURSOR (IL-3) (P-CELL STIMULATING FACTOR)
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                                       SUBUNIT: MONOMER.
TISSUE SPECIFICITY: ACTIVATED T CELLS, MAST CELLS, NATURAL KILLER
                                                                                                                                       FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES, FUNCTION: THIS CSF INDUCES GRANULOCYTES, MACROPHAGES, MAST CELLS,
SUBCELLULAR LOCATION: SECRETED.
                                                                                                                     STEM CELLS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
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(REL. 01, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDAT
                                                                                                               ERYTHROID
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                                                                                                                                    MAST CELLS
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SIMILARITY: BELONGS TO THE IL-3 FAMILY.

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EMBL; KO233; G387385; -.
EMBL; XO2732; G52674; -.
EMBL; M20128; G387387; -.
EMBL; M14394; G387387; JOINED.
EMBL; K01668; G387421; -.
       NOTEBOOM J.L., BOUT A.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

I- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOLESIS BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.

-I- FUNCTION: THIS CSF INDUCES GRANULOCYTES, MACROPHAGES, MAST CELLS, STEM CELLS, ERYTHROID CELLS, EOSINOPHILS AND MEGAKARYOCYTES.

-I- SUBUNIT: MONOMER.
-I- SISSUE SPECIFICITY: ACTIVATED T CELLS, MAST CELLS, NATURAL KILLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                    MEDLINE; 86232609.

COHEN D.R., HAPEL A.J., YOUNG I.G.;

"Cloning and expression of the rat interleukin-3
"UCCLEIC ACIDS RES. 14:3641-3658(1986).
                                                                                                                                                                                                                                                                                                                     INTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING FACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR) (MGSF-CELL GROWTH FACTOR) (MGGF).
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                                                                                                                                                 SEQUENCE FROM N.A. ESANDI M.C., VAN S
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      RODENTIA; SCIUROGNATHI; MURIDAE;
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EUKARYOTA; METAZOA; CHOI
                                                                                                                                                                                                                                                                                                                IL3 OR IL-3
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3-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
5-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
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IHI; MURIDAE; MURINAE;
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Pred. No. 3.2e-12;
0; Mismatches 0;
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RATTUS.
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EMBL; X03914; E10390; -...
EMBL; X03914; E10391; -...
EMBL; X03914; E10392; -...
EMBL; V03914; E10392; -...
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CARBOHYD
SEQUENCE
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01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDAT
FLAGELLAR BIOSYNTHESIS PROTEIN FLHA.
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P35620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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-1- SIMILARITY: BELONGS TO THE IL-3
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82.1%;
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6B571582 CRC32;
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"Bacillus subtilis FlhA: a flagellar protein "Bacillus subtilis FlhA: a flagellar protein of signal-transducing receptors"; or signal-transducing receptors "; or mrcrobiol, 7:735-743(1993).
between the Swiss Institute of Bloinf, the European Bioinformatics Institute use by non-profit institutions as 10 modified and this statement is not remmentally and the statement in the statement is not remmentally and the statement in the statement is not remmentally and statement in the state
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                                                                                                                                                                                                                                                                                                                                                                                                . MICROBIOL. 7:735-743(1993).
FUNCTION: INVOLVED IN THE EXPORT OF FLAGELLUM SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEI SIMILARITY: BELONGS TO THE FHIPEP (FLAGELLA/HE EXPORT PORE) FAMILY.
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EMBL; X63698; G39917; EMBL; Z99112; E118523(PIR; S33664; S33664.

BG10542;

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                                              U3M_HORSE
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Best Local Similarity
Matches 13; Conser
NU3M_HORSE STANDARD;
P48654;
01-FEB-1996 (REL. 33, CREATED)
                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                               EMBL; X97337; E237860;
PFAM; PF00507; oxidored
                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
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SEQUENCE
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).
MYND3 OR ND3 OR NADH3.
EQUUS ASINUS (DONKEY).
                                                                                                                                                                                                                                                                                                                                                                                                           UX., GULLBERG A., ARNASON U.;
The complete mitochondrial DNA (mtDNA) of the donkey and mtDNA;
comparisons among four closely related mammalian species-pairs.";
f. MOL. EVOL. 43:438-463(1996).
CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
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TRANSMEM
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PERISSODACTYLA; EQUIDAE; EQUUS.
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10; Conservative
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; NAD; UBIQUINONE; MITOCHONDRION
; AA; 13030 MW; B3B0653D CRC32;
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Pred. No. 5.8;
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RESULT 6
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Best Local (
EMBL; Y07726; E275046; PFAM; PF00507; oxidore
                                                                     the European Bioinformatics Institute. The Description of the property institutions as long modified and this statement into the moved entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                      NU3M_CERSI
003202;
                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CERATOTHERIUM SIMUM (WHITE RHINOCEROS) (SQUARE-LIPPED MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                          "The complete mitochondrial DNA sequence of the white rhinoceros, Ceratotherium simum, and comparison with the mtDNA sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                               XU X., ARNASON U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTND3 OR ND3 OR NADH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X79547; G577579; -
PFAM; PF00507; oxidored_q4; 1.
OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION
SEQUENCE 115 AA; 13016 MW; C4C238F9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERISSODACTYLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
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01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              email to license@isb-sib.ch).
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IYLA; EQUIDAE; EQUUS.
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Pred. No. 1.6;
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                                                                                            (See http://www.isb-sib.ch/announce,
                                                                                                                                                   There are no rest
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MITOCHONDRION.
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; J
NEWYONACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE;
                                                                                                                                                                                                                                                                                                      SHEEP
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                                                                                                   OVIS ARIES (SHEEP).
                                                                                                                             MIND3 OR ND3.
                                                                                                                                          15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDAT
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.3).
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SEQUENCE 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete mitochondrial DNA sequence of the greater Indian ceros, Rhinoceros unicornis, and the Phylogenetic relationship Carnivora, Perissodactyla, and Artiodactyla (+ Cetacea)."; BIOL. EVOL. 13:1167-1173(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; UBIQUINONE; MITOCHONDRION. 13044 MW; 9FE83B49 CRC32;
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Pred. No. 2
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                                                                                                                                                                         UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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EMBL; M59705; G168027;

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                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-slb.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF010406; G3445514; -
OXIDOREDUCTASE; NAD; UBIQUII
SEQUENCE 115 AA; 13102 M
                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                    membrane-spanning protein.";
J. BIOL. CHEM. 265:16132-16137(1990)
                                                                                                                                                                                                                                                                                                                                                              ENGLE D.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                               EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).
EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIME
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-|- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.
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                                                                                                                                                                                                                                                                                                                            A negative regulator of mitosis in Aspergillus is a putative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
                                                                                                                                                                                                              FUNCTION: NEGATIVE REGULATOR OF MITOSIS IN E.NIDULANS. THIS PROTEIN IS PART OF A REGULATORY PATHWAY THAT INCLUDES THE NIMA PROTEIN KINASE. IT IS REQUIRED TO PREVENT PREMATURE ENTRY INTO MITOSIS. MUTATIONS TO THES PROTEIN BOTH CAUSE CELLS TO ENTER MITOSIS AND PREVENT THEM FROM LEAVING MITOSIS.

SIMILARITY: TO MOUSE TSG24 AND YEAST YNL172W.
                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through sen the Swiss_Institute_of Bioinformatics and the Ev
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21, LAST SEQUENCE UP
34, LAST ANNOTATION
R OF MITOSIS.
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50.0%;
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Best Local
                                                                              EMBL; U32785; G1574079;
EMBL; U26665; G1353258;
TIGR; HI1045; -.
                                                                                                                                                                                       use by non-profit institutions as lon-
modified and this statement is not remove
entities requires a license agreement (
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way
                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E., KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J., MCKENNEY K., SUTTON G., FITZHUGH W., FIRELDS C.A., GOCAYME J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., WITTERBACK T.R., HANNA M.C., NGUYEN D.T., SADDEK D.M., BRANDON R.C.
       RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OOSMORE: S.M., SHORTREED J.M., COLEMAN D.C., ENGLAND D.M., KLEIN M. Sequences of the genes encoding the A, B and C subunits of the semophilus influenzae dimethylsulfoxide reductase complex."; ENE 169:137-138(1996).

1- FUNCTION: TERMINAL REDUCTASE DURING ANAEROBIC GROWTH ON VARIOUS SULFOXIDE AND N-OXIDE COMPOUNDS. THE C SUBUNIT ANCHORS THE OTHER TWO SUBUNITS TO THE MEMBRANE AND STABILIZE THE CATALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSC_HAEIN STANDARD; PRT; 279 AA.
445002; Q48050;
01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ANNEROBIC DIMETHYL SULFOXIDE REDUCTASE CHAIN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDLINE; 96186920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRAIN-EAGAN /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whole-genome random sequencing and assembly of Haemophilus nfluenzae\ Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRAIN-RD / KW20; EDLINE; 95350630.
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ACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNITS (BY SIMILARITY).
SUBUNIT: THE COMPLEX CONSIST OF THREE (
REDUCTASE; DMSB, AN ELECTRON TRANSFER I
MEMBRANE ANCHOR PROTEIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY)
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10; Conservative
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                                               TRANSMEMBRANE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23
PERIPLASMIC (POTENTIAL).
POTENTIAL.
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Pred. No. 1e+02;
                                               INNER MEMBRANE
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                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOUGHERTY B.A., MERRICK J.M.,
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364 MIVEASLYYPHNSLMINLILFAVGLTAFYS 393

1 MVLASSTTSIHTMLLLLLMLFHLGLQASIS 30

Query Match Best Local s Matches 11

Similarity

32.4%;

Score 45; Pred. No.

DB 1;

Length 574;

Mismatches

12;

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Conservative

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Best Local Similarity
Matches 10; Conser
  PFAM; PFUUTUL,
OXIDOREDUCTASE;
574 p
                             EMBL; U24570; G984298;
PFAM; PF00361; oxidored
PFAM; PF00662; oxidored
                                                                             entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                           MITOCHONDRION.
EUKARYOTA; METAZOA; ANNELIDA; CLITELLATA; OLIGOCHAETA; HAPLOTAXIDA;
LUMBRICINA; LUMBRICIDAE; LUMBRICUS.
                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (REL. 3
15-JUL-1998 (REL. 3
15-JUL-1998 (REL. 3
                                                                                                                                             This SWISS-PROT entry is copyright. It is produ
between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                         BOORE J.L., BROWN W.M.;
                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                 'Complete sequence of umbricus terrestris."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                UMBRICUS TERRESTRIS (COMMON EARTHWORM).
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oxidored_q1; 1.
oxidored_q1_N; 1.
oxidored_q1_N; 1.
; NAD; UBIQUINONE; MITOCHONDRION
AA; 64325 MW; 82ADABEE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No.
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T -> A (IN STRAIN EAGAN)
4A8DA212 CRC32;
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                                                                                                                                             It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                           574 AA
                                                                                        (See http://www.isb-sib.ch/announce/
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23;
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IL3_SAGOE
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Best Local Similarity
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IL3_CALJA
Q28334;
15-DEC-1998 |
IL3_SAGOE
P51445;
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrict use by non-profit institutions as just scontent is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib-entities requi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     World
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BIOCHIM. BIOPHYS. ACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BURGER H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CALLITHRIX JACCHUS (COMMON MARMOSET).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X74877;
                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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EDLINE; 94153996.
URGER H., MOSTERT M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIMATES; PLATYRRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAST-CELL GROWTH FACTOR) (MCGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-DEC-1998 (REL. 37, CREATED)
5-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
5-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
5-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
NTERLEUKIN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL
ACTOR) (HEMATOPOIETIC GROWTH FACTOR) (P-CELL 1)
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SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: MONOMER (BY SIMILARITY)
TISSUE SPECIFICITY: ACTIVATED T
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                                                                                                                                                                  HTMLLLLLMLFHLGLQAS
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INTERLEUKIN-3.
BY SIMILARITY.
POTENTIAL.
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                   PRT;
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                                                                                                                                                                                                                                                   Length 142;
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                                                                                                                                                                                                           Indels
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Best Local :
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE CYTOKINES THAT ACT IN HEMATOPOLESIS BY CONTROLLING THE PRODUCTION, DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES MACROPHAGES.
-I- FUNCTION: THIS CSF INDUCES GRANULOCYTES, MACROPHAGES, MAST CELLS, STEM CELLS, ERYTHROID CELLS, EOSINOPHILS AND MEGAKARYOCYTES.
-I- SUBUNIT: MONOMER (BY SIMILARITY).
         P51940;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELLS (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: SECRETED.
-1- SIMILARITY: BELONGS TO THE IL-3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAGUINUS OEDIPUS (COTTON-TOP TAMARIN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; PLATYRRHINI; CALLITRICHIDAE; SAGUINUS.
                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BURGER H., WAGEMAKER G., LEUNISSEN J.A.M., DORSSERS L.C. "Molecular evolution of interleukin-3.";
J. MOL. EVOL. 39:255-267(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and expression 
World monkeys.";
                                                                 NU3M_DROSU
                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                 HLPILLLLLVSPGLQAA 20
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                                                                                                                                                                                                 Similarity
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1998 (REL. 37, LAST ANNOTATION UPDATE)
18IN-3 PRECURSOR (IL-3) (MULTIPOTENTIAL COLONY-STIMULATING
1 (HEMATOPOIETIC GROWTH FACTOR) (P-CELL STIMULATING FACTOR)
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E211706; JOINED.
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POTENTIAL.
#### B2C52180 CRC32;
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INTERLEUKIN-3.
BY SIMILARITY.
                                                                                                                                                                                                Score 44;
Pred. No.
                                                                                                                                                                                     Mismatches
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                                                                 117
UPDATE)
3 (EC 1.6.5.3).
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                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                                                                                                                               SIGNAL
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OXIDOREDUCTASE

CHAIN

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Query Match
Best Local Similarity
Matches 9; Conserv
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WEDLINE; 98241181.

JANSSEN J.W.G., SCHLEITHHOFF L., BARTRAM C.R., SCHULZ A.S.;

JANSSEN J.W.G., SCHLEITHHOFF L., BARTRAM C.R., SCHULZ A.S.;

JANSSEN J.W.G., SCHLEITHHOFF L., BARTRAM C.R., SCHULZ A.S.;

An oncogenic fusion product of the phosphatidylinositol 3-kinase
p85beta subunit and HUMORF8, a putative deubiquitinating enzyme.";

ONCOGENE 16:1767-1772(1998).

-I- FUNCTION: BINDS TO ACTIVATED (PHOSPHORYLATED) PROTEIN-TYROSINE
KINASES, THROUGH ITS SH2 DOMAIN, AND ACTS AS AN ADAPTER, MEDIZATING
THE ASSOCIATION OF THE P110 CATALYTIC UNIT TO THE PLASMA MEMBRANE.

THE ASSOCIATION OF THE P110 (CATALYTIC) AND A P85 (REGULATORY)
                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLYBASE; FBgn0012957; Dsub\mt:ND3.

PFAM; PF00507; oxidored_q4; 1.

OXIDOREDUCTASE; NAD; UBIQUINONE; MITOCHONDRION.

SEQUENCE 117 AA; 13427 MW; B8EE2F7A CRC32;
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5-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
5-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
5-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
HOSPHATIDYLINOSITOL 3-KINASE REGULATORY BETA
185-BETA SUBUNIT) (PTDINS-3-KINASE P85-BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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DROSOPHILA SUBOBSCURA (FRUIT FLY).
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PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
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                             European Bioinformatics Institute.
                                                                                                                                                              SIMILARITY: CONTAINS 2 SH2 DOMAINS.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 1 RHO GAP DOMAIN.
SIMILARITY: HIGH, WITH OTHER P85-BETA SUBUNITS, AND ALSO TO
                                                                                                                                                  P85-ALPHA SUBUNIT
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Q90286 carassius a
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Q34191;
Q1-NOV-1996
Q1-NOV-1998
               SEQUENCE FROM N.A.

MEDLINE; 85079995.

LA CRUZ V.F., NECKELMANN N., SIMPSON I
"Sequences of six genes and several of
kinetoplast maxicircle DNA of Leishman
J. Biol. Chem. 259:15136-15147(1984).
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SEQUENCE 437
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Submitted (AUG-1991) to tl
EMBL; X56015; CAA39491.1;
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Submitted (OCT-1990)
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                                                                                                                                                                                                                              Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 01, Last sequence up (TrEMBLrel. 08, Last annotation OGENASE SUBUNIT 4.
                                                                                                                                                                                                                                                                                                                                     (Tremblrel. 01, Last sequence up
(Tremblrel. 08, Last annotation
WONE OXIDOREDUCTASE CHAIN 4 (EC.
                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58
58
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                                                                                                                                                                                                                                                                                 (Sauroleishmania
                                                                                                                                                                                                                     Kinetoplastida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinetoplastida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , GWANG II K., KOLESNIKOV
the EMBL/GenBank/DDBJ dat
1; -
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                                          several open
of Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50.5;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51;
Pred. No.
                                                                                                             SIMPSON L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ဖ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         741F2793 CRC32;
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                                                                                                                                                                                                                 Trypanosomatidae;
                                                                                                                                                                                                                                                                           tarentolae).
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                                             reading fra tarentolae.
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1.6.5.3).
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databases
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                                                                               frames
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Best Local s
Matches 9
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Best Local S
Matches 11
                                   086662 PRELIMI
086662
01-NOV-1998 (TIEMBI
01-NOV-1998 (TIEMBI
01-NOV-1998 (TIEMBI
01-NOV-1998 (TIEMBI
PUTATIVE INTEGRAL M
SC4A2.06C
                                                                                                                                                                                                                                                                                                                                Eukaryota; Meta
Pterygota; Dipt
Drosophilidae;
                                                                                                                                                                                                                     PFAM; PFO
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcripts from Leishmania tarentolae.";
Nucleic Acids Res. 13:5977-5993(1985).
-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE -
-!- COFACTOR: FAD, AND IRON-SULFUR CENTRES.
EMBL; M10126; -; NOT_ANNOTATED_CDS.
EFAM; PF00361; Oxidored_q1; 1.
                  Streptomyces coelicolor. Bacteria; Firmicutes; Ac
                                                                                                                                                                                                                                                                                            BHANOT P., BRINK M.,
                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1997
01-FEB-1997
                                                                                                                                                                                                                                      FLYBASE;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
MEDLINE; 96353971
                                                                                                                                                                                                                                                                                                                                                            Drosophila
                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; SEQUENCE 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 8529
SIMPSON A.G.,
         Actinomycetales;
                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                         Nature
                                                                                                                                                                                                                                                                    Wingless
                                                                                                                                                                                                                                                                                                                                                                                                                          094916
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                                                                                                                                   LLLRESSIGPHSCILVFLLIYFFGMASSI
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                                                                                                                                                    MVLASSTTSIHTMLLLLLMLFHLGLQASI
                                                                                                                                                                                                                                       U65589; AAC47273.1;
SE; FBgn0016797; fz2.
                                                                                                                                                                                                                               PF01392;
                                                                                                                                                                                                                                                382:225-230(1996).
                                                                                                                                                                       9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                     , NATHANS
                                                                                                                                                                                                                                                                                                                                         Metazoa;
Diptera;
                                                   B (Tremburel.
B (Tremburel.
B (Tremburel.
                                                                                                                                                                                                                                                                                                                                                           melanogaster
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(TrEMBLrel.
(TrEMBLrel.
                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                Drosophila.
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      Streptomycineae;
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                                           UIrel. 08, Created)
SUrel. 08, Last sequence update)
SUrel. 08, Last annotation update)
MEMBRANE PROTEIN.
                                                                                                                                                                                                              1.
: 75437 MW;
                                                                                                                                                                                                                                                                                                                                       aster (Fruit f
Arthropoda;
Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Ubiquinone; Mitochondrion;
52291 MW; EFF35AF7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              determination
                                                                                                                                                                                 34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.9%;
                                                                                                                                                                                                                                                                                             SAMOS
     Actinobacteria; Actinobacteridae; streptomyces
                                                                                                                                                                                                                                                                                   AMOS C.H.,
NUSSE R.;
                                                                                                                                                                                                                                                                                                                                                                                     102
                                                                                                                                                                                                                                             .•
                                                                                                                                                                     Score 48; DB Pred. No. 35; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence up
Last annotation
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Pred.
                                                                                        PRT;
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1; Tracheata; He
1; Muscomorpha;
                                                                                                                                                                                                                                                                          family
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                                                                                                                                                     29
                                                                                       344
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kinetoplast
                                                                                                                                                                                                                                                                                                                                                                                                                         694
                                                                                                                                                                               DB
35;
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                                                                                                                                                                                                                                                                                             WANG
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                                                                                                                                                                                                                                                                                                                                        Ephydroidea;
                                                                                                                                                                                         Length 694;
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                                                                                                                                                                       Indels
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Query Match
Best Local S
Matches 16
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Best Local S
Matches 13
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01-NOV-1996
01-MAY-1999
     01-JAN-1998
01-JAN-1998
                                             029705
                                                                                                                                                                                                                                                                                                              WAKELA T.P., HELLSTEN E., VESA J., HIRVONEN H., PALOTIE A., PELTONEN L., ALITALO K., ALITALO K.;
The rearranged L-myc fusion gene (RLF) encodes a Zn-15 related
                                                                                                                                                                                                                                                                                                                                                                                    S. .
Jomo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                   ROSITE; PS00028; ZINC_FINGER_C2H2; 14
                                                                                                                                                                                                                                                                                           ncogene 11:2699-2704(1995).
                                                                                                                                                                                                                                                                                                                                                                EDLINE;
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                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
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                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAIN=A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NASHI H., HOPWOOD D.A.;
set of ordered cosmids and a detailed genetic
e 8 Mb Streptomyces coefficolor A3(2) chromosome
1. Microbiol. 21:77-96(1996).
BL; ALO31182; CAA20158.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LASSTTSIHTM-LLLLLMLFHLGLQASI 29
                                                                                                     SSESSICASKRPCTEDTMLELLLRLKHLSLKNSIT 1077
                                                                                                                                     SSTTSI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPPSHLTLHTAPLLLSLVLFSAGLQVPV 67
                                                                                                                                                                                                                                                                  U22377; AAC50396.1;
PF00096; zf-C2H2; 1
                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 46.4
13; Conservative
                                                                                                                                                                                                                                                                                                                                                              96132723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AUG-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TIEMBLIEL 01, Created)
(TIEMBLIEL 01, Last sequence update)
(TIEMBLIEL 10, Last annotation update)
    (TrEMBLrel.
                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                          Metal-binding; DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIESER H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FINGER PROTEIN
                                                                                                                             -HTMLLLLLMLFHLGLQASIS
                                                                                                                                                                       34.2%;
45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.2%;
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  Last
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EMBL/GenBank/DDBJ databases.
               Created)
                                                                                                                                                        Score 47.5; [
Pred. No. 98;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47.5; D
Pred. No. 23;
4; Mismatches
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sequence update)
                                                                                                                                                                                                                         05EBE74D CRC32;
                                      244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome
                                      A.
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                                                                                                                                                                                 DB 4;
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                                                                                                                                                                                 Length 1914;
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                                                                                                                                                        Indels
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Matches 10
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Best Local
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                                                                                                           DNA Res.
                                                                                                                                                                     YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAM
SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSI
                                                                                                                                                                                                                                                                                                                                                                                                                         058301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 244 AA; 27573 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PETERSON S., REICH C.I., MCNEIL I.K., BADGER J.H., GLODEK J. OVERBEEK R., GCCAXNE J.D., WEIDMAN J.F., MCDONALD L., UTTER COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYRES S.M. SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.P. SADOW T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.
                                                                                                                                                                                                                           CAWARABAYASI Y.,
                                                                                                                                                                                                                                                                                                                 yrococcus horikoshii.
                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
11-JAN-1999 (TrEMBLrel. 09, Last annotation updat
160AA LONG HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                             25830
                                                                                                                Complete sequence and gene organization of the genome of a year-thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE00
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                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haeoglobus fulgidus.
haea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILAMLFHIGLIVSLS 103
                  Similarity
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9; Conser
                                                                                                      5:55-76(1998)
                                                                                                                                                                                                                                         98344137.
                                                                                                                                                                                                                                                                                                  Euryarchaeota;
                                                                                                                                                                 NAKAMURA Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          066; AAB90687.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                           BAA29655.1; -
VA; 18153 MW;
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                                                                                                                                                                                                         SAWADA M., HORIKAWA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAMMA
                45.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaeoglobales;
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Fred. No. 14;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
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                                                                        7E023984 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                            HORIKOSHI
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             DB
14;
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                             Length 160;
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                                                                                                                                                            SHIZUYA
                                                                                                                                                                          OGUCHI
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(TrEMBLrel. 10, PRELIMINARY;

PRT;

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Best Local Similarity 44.
Matches 12; Conservative
                                              KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E., KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.I. RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHMANN R.D., QUACKENNUSH J., LEE N.H., SUTTON G.G., GILL KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUN PETERSON S., REICH C.I., MCNEIL L.K., BAGGER J.H., GLODEK A., OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM SECURINE, 99097286.

KIM K.S., LEE S.E., JEONG H.W., HA J.H.;

"The complete nucleotide sequence of the familiaris) mitochondrial genome.";

"All Phylogenet. Evol. 10:210-220(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9ZZ60
Q9ZZ60;
Q1-MAY-1999
Q1-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                          030142;
sulphate-reducing archaeon Archaeoglobus
                                                                                                                                                                                                                 STRAIN-VC-
                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TIEMBLIEL. 05, Created)
01-JAN-1998 (TIEMBLIEL. 05, Last sequence update)
01-JUG-1998 (TIEMBLIEL 07, Last annotation updat
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                              STRAIN-VC-16 / DSM 4304
MEDLINE; 98049343.
                                                                                                                                                                                                                                                                       Archaeoglobus fulgidus.
Archaea; Euryarchaeota;
                                        ENTER J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion.
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IM K.S., LEE S.E.,
ubmitted (APR-1997)
                       he complete genome sequence
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 10, Last annotation updat
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12937
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                                                                                                                                                                                                              ATCC 49558;
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Pred.
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ia; Canidae;
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                       the hyperthermophilic,
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12;
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       fulgidus.";
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Best Local S
Matches 7
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Best Local S
Matches 9
                                   BONFIELD J. BURTON J., CONNELL M., COPERY T., COOPER J., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOH JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P. LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., OARD R., SULSTON J. SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J. THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERST
                                                                                                                                                                                                                                               P91486; PRELIMINARY;
P91486; O1-MAY-1997 (TIEMBLEEL 03,
01-MAY-1997 (TIEMBLEEL 03,
01-NOV-1998 (TIEMBLEEL 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P96480;
P96480;
01-MAY-1997
01-MAY-1997
01-AUG-1998
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Hypothetical
SEQUENCE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUNOZ R., MOLLERACH M.E., LOPEZ
MO1. Microbiol. 25:79-92(1997).
EMBL, Z83335; CABO5927.1;
Hypothetical protein.
SEQUENCE 346 AA; 39177 MW; A
                                                                                                                     MEDLINE; 94150718.
WILSON R., AINSCOUGH R.,
BONFIELD J., BURTON J.,
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                           Rhabditina;
                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
                                                                                                                                                                                                                                         SIMILARITY TO QUAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MUNOZ R., MOLLERACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae.
Bacteria; Firmicutes; Bac
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7 (TremBirel. 03, La
8 (TremBirel. 07, La
NL 39.2 KD PROTEIN.
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342 AA; 38629 MW;
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                                                                                                                                                                                       Nematoda; Secernentea; Rhabditia; Rhabditida;
Didea; Rhabditidae; Peloderinae; Caenorhabditis,
                                                                                                                                                                                                                                         NEURONAL
                                                                                                                                                                                                                                                                                                                                                         113
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                                                                                                                                                                                                                                                                                                                                                                                                                33.1%;
50.0%;
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                                                                                                                                 ANDERSON K.,
                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
L CELL CYCLE WITHDRAWAL
                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB Pred. No. 37; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
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Pred. No. 36;
8; Mismatches
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                                                                                                                     COPSEY T., COOPER
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                                                                       O'CALLAGHAN M.,
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                                                                                             JOHNSTON L.,
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Best Local Similarity 36./
11; Conservative
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Best Local Similarity 45.:
Matches 15; Conservative
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
DU 2., MAGGI L.;
Submitted (JAN-1997) t
        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                01-NOV-1996 (TrEMBLrel 01-NOV-1996 (TrEMBLrel 01-MAY-1999 (TrEMBLrel 01-MAY-1999 (TrEMBLrel 01-MAY-1999 (TremBLrel 01-NOV-1996 (TremBLrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUDMILTER H., HARTMANN C.M., SUDMILTEE (NOV-1997) to the EMBL; L26308; AAA30978.1; ... EMBL; AJ003021; CAA05806.1; SEQUENCE 653 AA; 70551 Mr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WATERSTON R.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U80440; AAB37650.1; -
SEQUENCE 414 AA; 46525 MW; EB685192 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 ILLAGSLTLLCTCLILLVKLLNSVLQGQVA 384
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STRAIN-BRISTOL N2;
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SSUE-EPITHELIUM, KIDNEY;
EDLINE; 94165050.
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karyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
statheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSUE-KIDNEY;
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-NOV-1998 (TrEMBLrel.
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Biol. Chem. 269:6615-6621(1994).
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                                                                                                                                         PROTEIN.
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EMBL/GenBank/DDBJ databases.
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Pred. No. 63;
8; Mismatches
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Pred. No. 43;
6; Mismatches
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63;
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PFAM; PF00503; G-alpha; 1.
SEQUENCE 352 AA; 41021 MW;
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Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                10 IHTMLLLLMLFHLGLQ 26
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                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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1999, 20:40:13
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Pred. No.
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Search completed: September 16, Job time: 5564 sec